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```
     Inversion start site
     |
     ATTATAAAGGAAAAAGAAAATAACGCAATGGACAAGTGGTG
860  +---------+---------+---------+---------+  900
     TAATATTTCCTTTTTCTTTTATTGCGTTACCTGTTCACCAC  (41)
       Y  K  G  K  R  K  *  R  N  G  Q  V  V

     AAGCTGTGAACTCAGGTGTGCACAATTATCAGGAACACCCCAAAACCAAAGTGAGGTAGA
901  ---------+---------+---------+---------+---------+---------+  960
     TTCGACACTTGAGTCCACACGTGTTAATAGTCCTTGTGGGGTTTTGGTTTCACTCCATCT  (101)
     K  L  *  T  Q  V  C  T  I  I  R  N  T  P  K  P  K  *  G  R

     AATAGCATGAGAAGCCGTGTTTGATGTTAATTAATT
961  ---------+---------+---------+------  996
     TTATCGTACTCTTCGGCACAAACTACAATTAATTAA  (137)
     N  S  M  R  S  R  V  *  C  *  L  I
```

The inversion sequence of the apo-dystrophin-4 cDNA (SEQ ID NO: 1)

Figure 1

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```
              Inversion start site
                  |
     TAAAGAAAGAATTATAAAGGAAAAAGAAAATAACGCAATGGACAAGTGGTG
850  +---------+---------+---------+---------+---------+   900
     ATTTCTTTCTTAATATTTCCTTTTTCTTTTATTGCGTTACCTGTTCACCAC   (51)
     *  R  K  N  Y  K  G  K  R  K  *  R  N  G  Q  V  V

     AAGCTGTGAACTCAGGTGTGCACAATTATCAGGAACACCCCAAAACCAAAGTGAGGTAGA
901  ---------+---------+---------+---------+---------+---------+   960
     TTCGACACTTGAGTCCACACGTGTTAATAGTCCTTGTGGGGTTTTGGTTTCACTCCATCT   (111)
     K  L  *  T  Q  V  C  T  I  I  R  N  T  P  K  P  K  *  G  R

     AATAGCATGAGAAGCCGTGTTTGATGTTAATTAATT
961  ---------+---------+---------+------   996
     TTATCGTACTCTTCGGCACAAACTACAATTAATTAA (147)
     N  S  M  R  S  R  V  *  C  *  L  I
```

The inversion sequence of the apo-dystrophin-4 cDNA plus a 10 base-pair region 5' to the start of the inversion sequence (SEQ ID NO: 1A, included in SEQ ID NO: 2).

Figure 1A

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```
     Start at 710
     |
     AACAATGGCAG
     +---------+   720
     TTGTTACCGTC   (11)
       Q  W  Q

     GTTTTACACGTCTATGCAATTGTACAAAAAAGTTATAAGAAAACTACATGTAAAATCTTG
721  ---------+---------+---------+---------+---------+---------+   780
     CAAAATGTGCAGATACGTTAACATGTTTTTTCAATATTCTTTTGATGTACATTTTAGAAC   (71)
     V  L  H  V  Y  A  I  V  Q  K  S  Y  K  K  T  T  C  K  I  L

     ATAGCTAAATAACTTGCCATTTCTTTATATGGAACGCATTTTGGGTTGTTTAAAAATTTA
781  ---------+---------+---------+---------+---------+---------+   840
     TATCGATTTATTGAACGGTAAAGAAATATACCTTGCGTAAAACCCAACAAATTTTTAAAT   (131)
     I  A  K  *  L  A  I  S  L  Y  G  T  H  F  G  L  F  K  N  L
                inversion start site
                           |
     TAACAGTTATAAAGAAAGAATTATAAAGGAAAAAGAAAATAACGCAATGGACAAGTGGTG
841  ---------+---------+---------+---------+---------+---------+   900
     ATTGTCAATATTTCTTTCTTAATATTTCCTTTTTCTTTTATTGCGTTACCTGTTCACCAC   (191)
     *  Q  L  *  R  K  N  Y  K  G  K  R  K  *  R  N  G  Q  V  V

     AAGCTGTGAACTCAGGTGTGCACAATTATCAGGAACACCCCAAAACCAAAGTGAGGTAGA
901  ---------+---------+---------+---------+---------+---------+   960
     TTCGACACTTGAGTCCACACGTGTTAATAGTCCTTGTGGGGTTTTGGTTTCACTCCATCT   (251)
     K  L  *  T  Q  V  C  T  I  I  R  N  T  P  K  P  K  *  G  R

     AATAGCATGAGAAGCCGTGTTTGATGTTAATTAATT
961  ---------+---------+---------+------   996
     TTATCGTACTCTTCGGCACAAACTACAATTAATTAA (287)
     N  S  M  R  S  R  V  *  C  *  L  I
```

The inversion sequence of the apo-dystrophin-4 cDNA plus the upstream 150 bp from the start of the inversion at 860 to the Hpa I enzyme site (SEQ ID NO: 1B, included in SEQ ID NO: 2)

Figure 1B

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```
       GTGGTTTGATTGATAGTAAAAAAAATGTTCGTTAATACAAGTAGAGAGTAAGTAATCAAT
     1 ---------+---------+---------+---------+---------+---------+ 60
       CACCAAACTAACTATCATTTTTTTTACAAGCAATTATGTTCATCTCTCATTCATTAGTTA
       V  V  *  L  I  V  K  K  M  F  V  N  T  S  R  E  *  V  I  N

       CAATCACTCATAGCCAAGGTGGAAAAGATGTATCCCATCATGGAATATTCCTGTTCTGAT
    61 ---------+---------+---------+---------+---------+---------+ 120
       GTTAGTGAGTATCGGTTCCACCTTTTCTACATAGGGTAGTACCTTATAAGGACAAGACTA
       Q  S  L  I  A  K  V  E  K  M  Y  P  I  M  E  Y  S  C  S  D

       AGAAATCTTGTGCTTATCTATGGAATTCTTTTGATATATATTTACATTGGGAACCTGAAT
   121 ---------+---------+---------+---------+---------+---------+ 180
       TCTTTAGAACACGAATAGATACCTTAAGAAAACTATATATAAATGTAACCCTTGGACTTA
       R  N  L  V  L  I  Y  G  I  L  L  I  Y  I  Y  I  G  N  L  N

       GTAGCTTGACATTTTTCCATGTAAACACCAGTAGCCTGATCCAACATTAAGCTGATACTA
   181 ---------+---------+---------+---------+---------+---------+ 240
       CATCGAACTGTAAAAAGGTACATTTGTGGTCATCGGACTAGGTTGTAATTCGACTATGAT
       V  A  *  H  F  S  M  *  T  P  V  A  *  S  N  I  K  L  I  L

       ACAAACAACGTGTAATGGCTTCATTAATAAGGCTTTGCTTCTTCCTGGAAACTGGTGAAA
   241 ---------+---------+---------+---------+---------+---------+ 300
       TGTTTGTTGCACATTACCGAAGTAATTATTCCGAAACGAAGAAGGACCTTTGACCACTTT
       T  N  N  V  *  W  L  H  *  *  G  F  A  S  S  W  K  L  V  K

       AATCAAACCTTGTTGTGTACACCCTCGATGCAGCTTCTGTGTTGTCTTCACCCAGAAATG
   301 ---------+---------+---------+---------+---------+---------+ 360
       TTAGTTTGGAACAACACATGTGGGAGCTACGTCGAAGACACAACAGAAGTGGGTCTTTAC
       N  Q  T  L  L  C  T  P  S  M  Q  L  L  C  C  L  H  P  E  M
```

The polynucleotide sequence of apo-dystrophin-4 (SEQ ID NO: 2)

Figure 2

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```
      GGGAATGATTTCCCAAATGGCAAAGAAACAGAGTGATGCTATCTATCTGCACCTTTTGTA
361   ---------+---------+---------+---------+---------+---------+   420
      CCCTTACTAAAGGGTTTACCGTTTCTTTGTCTCACTACGATAGATAGACGTGGAAAACAT
      G  N  D  F  P  N  G  K  E  T  E  *  C  Y  L  S  A  P  F  V

      AAGTCTGTCTTTCTTTCTCTTTGTTTTCCAGGACACAATGTAGGAAGTCTTTTCCACATG
421   ---------+---------+---------+---------+---------+---------+   480
      TTCAGACAGAAAGAAAGAGAAACAAAAGGTCCTGTGTTACATCCTTCAGAAAAGGTGTAC
      K  S  V  F  L  S  L  C  F  P  G  H  N  V  G  S  L  F  H  M

      GCAGATGATTTGGGCAGAGCGATGGAGTCCTTAGTATCAGTCATGACAGATGAAGAAGGA
481   ---------+---------+---------+---------+---------+---------+   540
      CGTCTACTAAACCCGTCTCGCTACCTCAGGAATCATAGTCAGTACTGTCTACTTCTTCCT
      A  D  D  L  G  R  A  M  E  S  L  V  S  V  M  T  D  E  E  G

      GCAGAATAAATGTTTTACAACTCCTGATTCCCGCATGGTTTTTATAATATTCATACAACA
541   ---------+---------+---------+---------+---------+---------+   600
      CGTCTTATTTACAAAATGTTGAGGACTAAGGGCGTACCAAAAATATTATAAGTATGTTGT
      A  E  *  M  F  Y  N  S  *  F  P  H  G  F  Y  N  I  H  T  T

      AAGAGGATTAGACAGTAAGAGTTTACAAGAAATAAATCTATATTTTTGTGAAGGGTAGTG
601   ---------+---------+---------+---------+---------+---------+   660
      TTCTCCTAATCTGTCATTCTCAAATGTTCTTTATTTAGATATAAAAACACTTCCCATCAC
      K  R  I  R  Q  *  E  F  T  R  N  K  S  I  F  L  *  R  V  V

      GTATTATACTGTAGATTTCAGTAGTTTCTAAGTCTGTTATTGTTTTGTTAACAATGGCAG
661   ---------+---------+---------+---------+---------+---------+   720
      CATAATATGACATCTAAAGTCATCAAAGATTCAGACAATAACAAAACAATTGTTACCGTC
      V  L  Y  C  R  F  Q  *  F  L  S  L  L  L  F  C  *  Q  W  Q
```

Figure 2 (cont'd)

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```
     GTTTTACACGTCTATGCAATTGTACAAAAAAGTTATAAGAAAACTACATGTAAAATCTTG
721  ---------+---------+---------+---------+---------+---------+  780
     CAAAATGTGCAGATACGTTAACATGTTTTTTCAATATTCTTTTGATGTACATTTTAGAAC
     V  L  H  V  Y  A  I  V  Q  K  S  Y  K  K  T  T  C  K  I  L

     ATAGCTAAATAACTTGCCATTTCTTTATATGGAACGCATTTTGGGTTGTTTAAAAATTTA
781  ---------+---------+---------+---------+---------+---------+  840
     TATCGATTTATTGAACGGTAAAGAAATATACCTTGCGTAAAACCCAACAAATTTTTAAAT
     I  A  K  *  L  A  I  S  L  Y  G  T  H  F  G  L  F  K  N  L

     TAACAGTTATAAAGAAAGAATTATAAAGGAAAAAGAAAATAACGCAATGGACAAGTGGTG
841  ---------+---------+---------+---------+---------+---------+  900
     ATTGTCAATATTTCTTTCTTAATATTTCCTTTTTCTTTTATTGCGTTACCTGTTCACCAC
     *  Q  L  *  R  K  N  Y  K  G  K  R  K  *  R  N  G  Q  V  V

     AAGCTGTGAACTCAGGTGTGCACAATTATCAGGAACACCCCAAAACCAAAGTGAGGTAGA
901  ---------+---------+---------+---------+---------+---------+  960
     TTCGACACTTGAGTCCACACGTGTTAATAGTCCTTGTGGGGTTTTGGTTTCACTCCATCT
     K  L  *  T  Q  V  C  T  I  I  R  N  T  P  K  P  K  *  G  R

     AATAGCATGAGAAGCCGTGTTTGATGTTAATTAATT
961  ---------+---------+---------+------  996
     TTATCGTACTCTTCGGCACAAACTACAATTAATTAA
     N  S  M  R  S  R  V  *  C  *  L  I
```

Figure 2 (cont'd)

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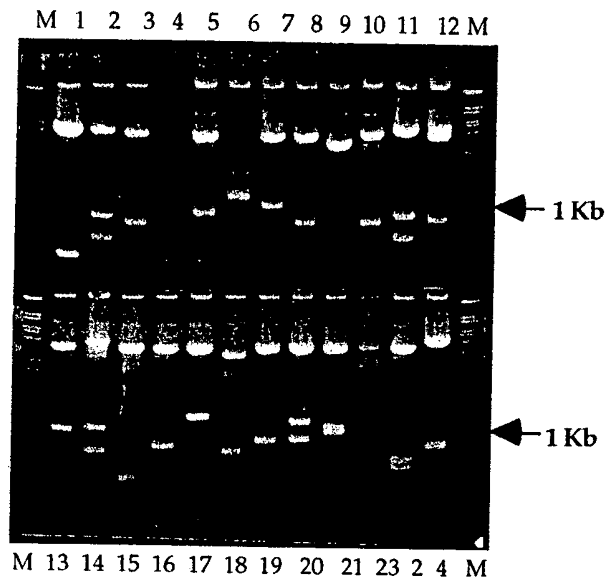

Figure 3A

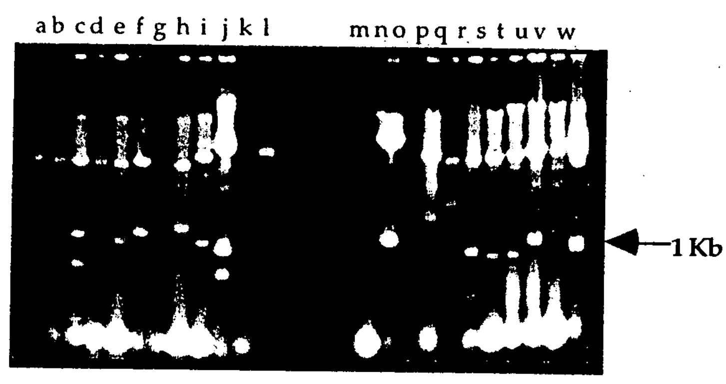

Figure 3B

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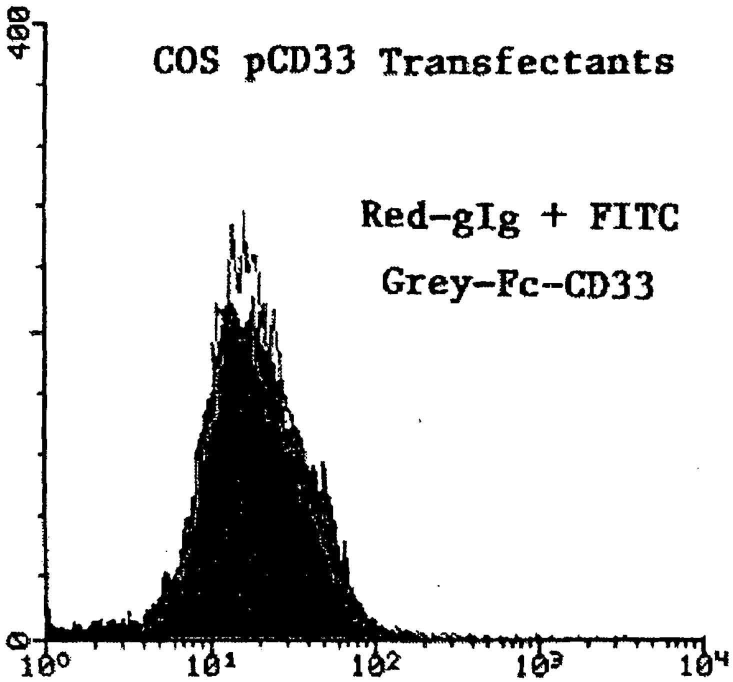

Figure 4A

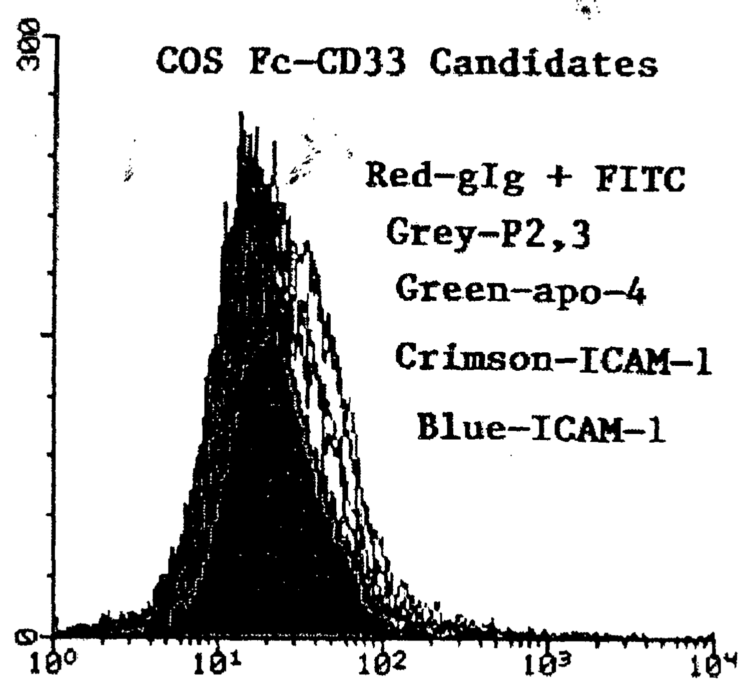

Figure 4B

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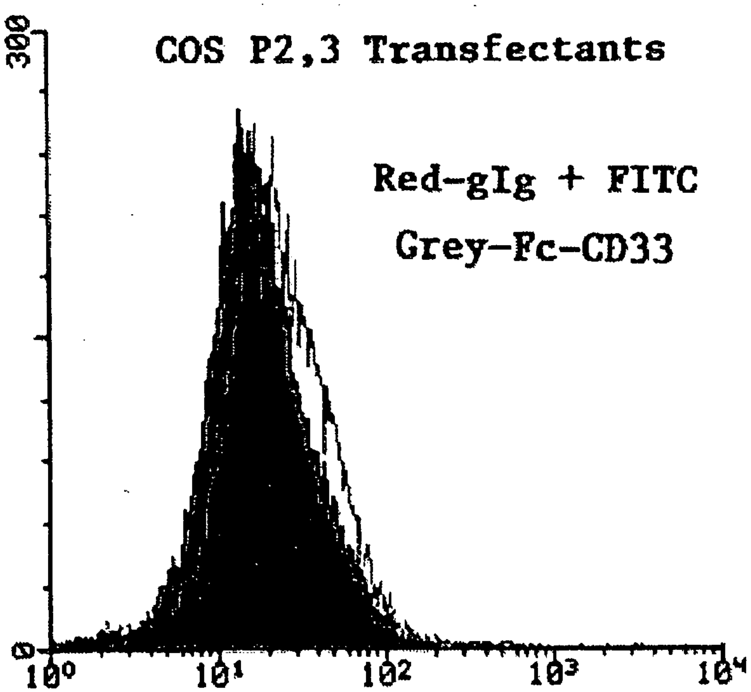

Figure 4C

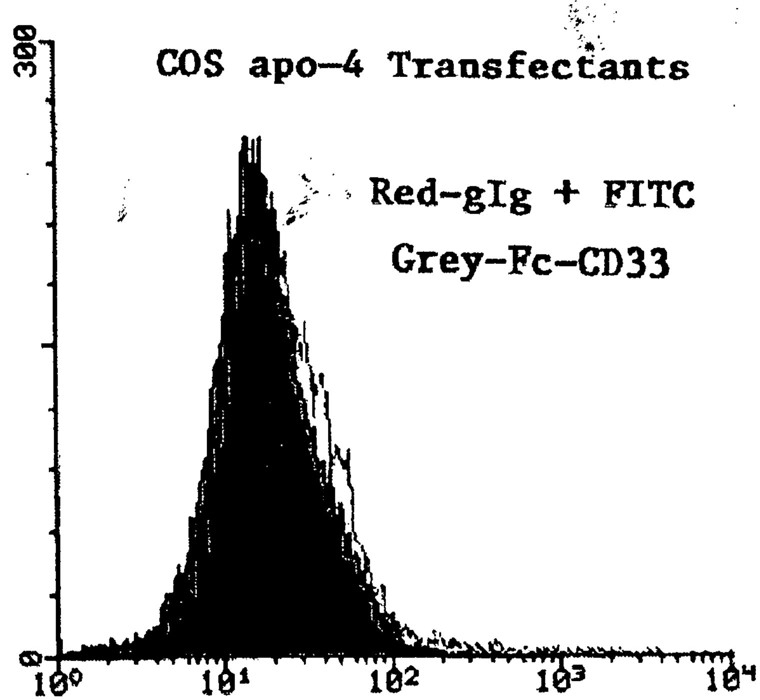

Figure 4D

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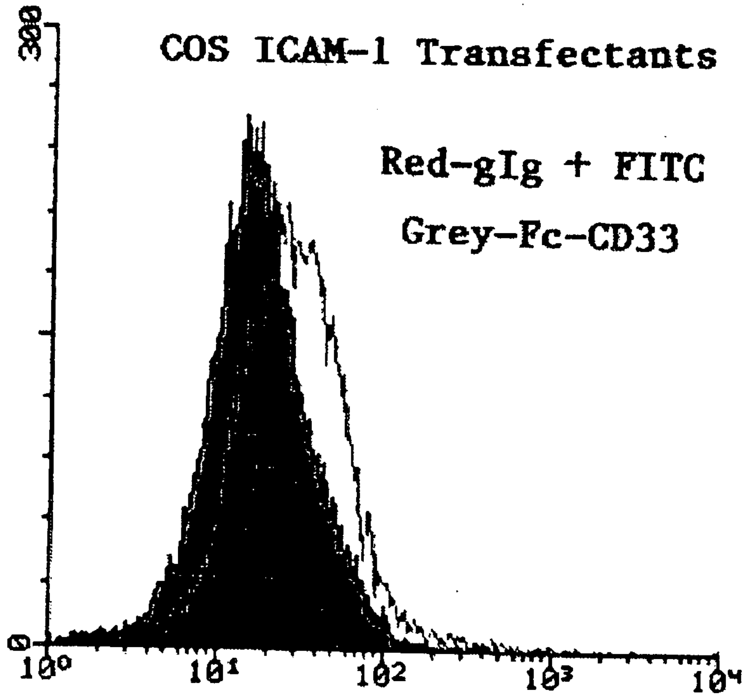

Figure 4E

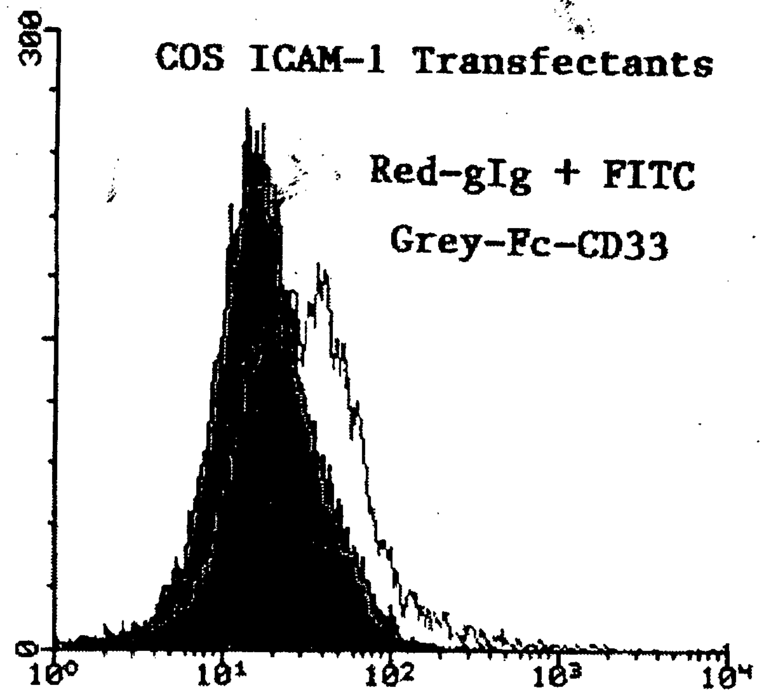

Figure 4F

OIPE JC132
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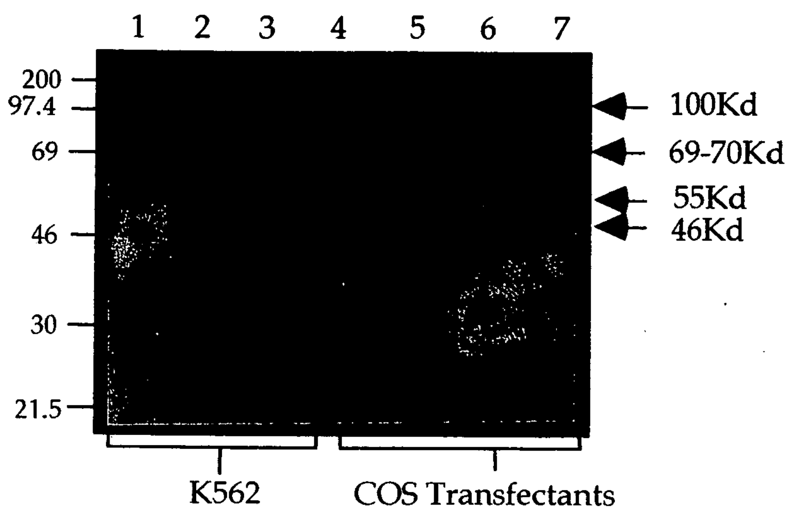

Figure 5

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```
     ...TAGTTTCCTATTCAATGTATAGTGCACCAAAGGTCAATTCAAGAGTTTATTATTATT
-239 ---------+---------+---------+---------+---------+---------+  -180
     ...ATCAAAGGATAAGTTACATATCACGTGGTTTCCAGTTAAGTTCTCAAATAATAATAA
     .  *  F  P  I  Q  C  I  V  H  Q  R  S  I  Q  E  F  I  I  I

     ATTTTCAACCCAAGTAAAAGCAGAGAGAAAATAGCCACCTCCACCATAGCCTCAGAAGCA
-179 ---------+---------+---------+---------+---------+---------+  -120
     TAAAAGTTGGGTTCATTTTCGTCTCTCTTTTATCGGTGGAGGTGGTATCGGAGTCTTCGT
     I  F  N  P  S  K  S  R  E  K  I  A  T  S  T  I  A  S  E  A

     AGCCAACAGCCTGAAACAGCTTTGAAATGAAAAGTTGGTGTGGCGGTGATGGTGGCAGTG
-119 ---------+---------+---------+---------+---------+---------+  -60
     TCGGTTGTCGGACTTTGTCGAAACTTTACTTTTCAACCACACCGCCACTACCACCGTCAC
     S  Q  Q  P  E  T  A  L  K  *  K  V  G  V  A  V  M  V  A  V

     ATAATGGTGACCGATGGTTGGGTGCTGGTGATGGTAGTGGTAGTTGTGAAGGTGGTGATG
 -59 ---------+---------+---------+---------+---------+---------+  0
     TATTACCACTGGCTACCAACCCACGACCACTACCATCACCATCAACACTTCCACCACTAC
     I  M  V  T  D  G  W  V  L  V  M  V  V  V  V  V  K  V  V  M

     GTGGTTTGATTGATAGTAAAAAAAATGTTCGTTAATACAAGTAGAGAGTAAGTAATCAAT
   1 ---------+---------+---------+---------+---------+---------+  60
     CACCAAACTAACTATCATTTTTTTTACAAGCAATTATGTTCATCTCTCATTCATTAGTTA
     V  V  *  L  I  V  K  K  M  F  V  N  T  S  R  E  *  V  I  N

     CAATCACTCATAGCCAAGGTGGAAAAGATGTATCCCATCATGGAATATTCCTGTTCTGAT
  61 ---------+---------+---------+---------+---------+---------+  120
     GTTAGTGAGTATCGGTTCCACCTTTTCTACATAGGGTAGTACCTTATAAGGACAAGACTA
     Q  S  L  I  A  K  V  E  K  M  Y  P  I  M  E  Y  S  C  S  D

     AGAAATCTTGTGCTTATCTATGGAATTCTTTTGATATATATTTACATTGGGAACCTGAAT
 121 ---------+---------+---------+---------+---------+---------+  180
     TCTTTAGAACACGAATAGATACCTTAAGAAAACTATATATAAATGTAACCCTTGGACTTA
     R  N  L  V  L  I  Y  G  I  L  L  I  Y  I  Y  I  G  N  L  N

     GTAGCTTGACATTTTTCCATGTAAACACCAGTAGCCTGATCCAACATTAAGCTGATACTA
 181 ---------+---------+---------+---------+---------+---------+  240
     CATCGAACTGTAAAAAGGTACATTTGTGGTCATCGGACTAGGTTGTAATTCGACTATGAT
     V  A  *  H  F  S  M  *  T  P  V  A  *  S  N  I  K  L  I  L

     ACAAACAACGTGTAATGGCTTCATTAATAAGGCTTTGCTTCTTCCTGGAAACTGGTGAAA
 241 ---------+---------+---------+---------+---------+---------+  300
     TGTTTGTTGCACATTACCGAAGTAATTATTCCGAAACGAAGAAGGACCTTTGACCACTTT
     T  N  N  V  *  W  L  H  *  *  G  F  A  S  S  W  K  L  V  K

     AATCAAACCTTGTTGTGTACACCCTCGATGCAGCTTCTGTGTTGTCTTCACCCAGAAATG
 301 ---------+---------+---------+---------+---------+---------+  360
     TTAGTTTGGAACAACACATGTGGGAGCTACGTCGAAGACACAACAGAAGTGGGTCTTTAC
     N  Q  T  L  L  C  T  P  S  M  Q  L  L  C  C  L  H  P  E  M
```

Figure 6 (SEQ ID NO: 51)

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```
    GGGAATGATTTCCCAAATGGCAAAGAAACAGAGTGATGCTATCTATCTGCACCTTTTGTA
361 ---------+---------+---------+---------+---------+---------+ 420
    CCCTTACTAAAGGGTTTACCGTTTCTTTGTCTCACTACGATAGATAGACGTGGAAAACAT
    G N D F P N G K E T E * C Y L S A P F V
                              begin exon 79
                                   |
    AAGTCTGTCTTTCTTTCTCTTTGTTTTCCAGGACACAATGTAGGAAGTCTTTTCCACATG
421 ---------+---------+---------+---------+---------+---------+ 480
    TTCAGACAGAAAGAAAGAGAAACAAAAGGTCCTGTGTTACATCCTTCAGAAAAGGTGTAC
    K S V F L S L C F P G H N V G S L F H M

    GCAGATGATTTGGGCAGAGCGATGGAGTCCTTAGTATCAGTCATGACAGATGAAGAAGGA
481 ---------+---------+---------+---------+---------+---------+ 540
    CGTCTACTAAACCCGTCTCGCTACCTCAGGAATCATAGTCAGTACTGTCTACTTCTTCCT
    A D D L G R A M E S L V S V M T D E E G

    GCAGAATAAATGTTTTACAACTCCTGATTCCCGCATGGTTTTTATAATATTCATACAACA
541 ---------+---------+---------+---------+---------+---------+ 600
    CGTCTTATTTACAAAATGTTGAGGACTAAGGGCGTACCAAAAATATTATAAGTATGTTGT
    A E * M F Y N S * F P H G F Y N I H T T

                                  (----N----)
    AAGAGGATTAGACAGTAAGAGTTTACAAGAAATAAATCTATATTTTTGTGAAGGGTAGTG
601 ---------+---------+---------+---------+---------+---------+ 660
    TTCTCCTAATCTGTCATTCTCAAATGTTCTTTATTTAGATATAAAAACACTTCCCATCAC
    K R I R Q * E F T R N K S I F L * R V V

    GTATTATACTGTAGATTTCAGTAGTTTCTAAGTCTGTTATTGTTTTGTTAACAATGGCAG
661 ---------+---------+---------+---------+---------+---------+ 720
    CATAATATGACATCTAAAGTCATCAAAGATTCAGACAATAACAAAACAATTGTTACCGTC
    V L Y C R F Q * F L S L L L F C * Q W Q

    GTTTTACACGTCTATGCAATTGTACAAAAAAGTTATAAGAAAACTACATGTAAAATCTTG
721 ---------+---------+---------+---------+---------+---------+ 780
    CAAAATGTGCAGATACGTTAACATGTTTTTTCAATATTCTTTTGATGTACATTTTAGAAC
    V L H V Y A I V Q K S Y K K T T C K I L

    ATAGCTAAATAACTTGCCATTTCTTTATATGGAACGCATTTTGGGTTGTTTAAAAATTTA
781 ---------+---------+---------+---------+---------+---------+ 840
    TATCGATTTATTGAACGGTAAAGAAATATACCTTGCGTAAAACCCAACAAATTTTTAAAT
    I A K * L A I S L Y G T H F G L F K N L
              inversion start site
                        |
    TAACAGTTATAAAGAAAGAATTATAAAGGAAAAAGAAAATAACGCAATGGACAAGTGGTG
841 ---------+---------+---------+---------+---------+---------+ 900
    ATTGTCAATATTTCTTTCTTAATATTTCCTTTTTCTTTTATTGCGTTACCTGTTCACCAC
    * Q L * R K N Y K G K R K * R N G Q V V
```

Figure 6 (cont'd)

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```
    AAGCTGTGAACTCAGGTGTGCACAATTATCAGGAACACCCCAAAACCAAAGTGAGGTAGA
901 ---------+---------+---------+---------+---------+---------+ 960
    TTCGACACTTGAGTCCACACGTGTTAATAGTCCTTGTGGGGTTTTGGTTTCACTCCATCT
    K  L  *  T  Q  V  C  T  I  I  R  N  T  P  K  P  K  *  G  R

    AATAGCATGAGAAGCCGTGTTTGATGTTAATTAATT
961 ---------+---------+---------+------ 996
    TTATCGTACTCTTCGGCACAAACTACAATTAATTAA
    N  S  M  R  S  R  V  *  C  *  L  I
```

Figure 6 (cont'd)

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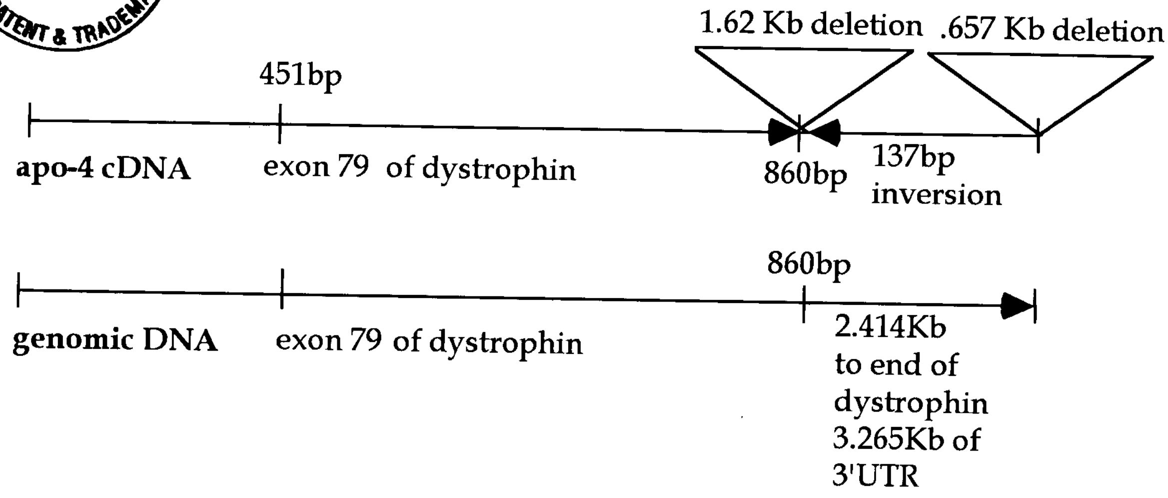

Figure 7

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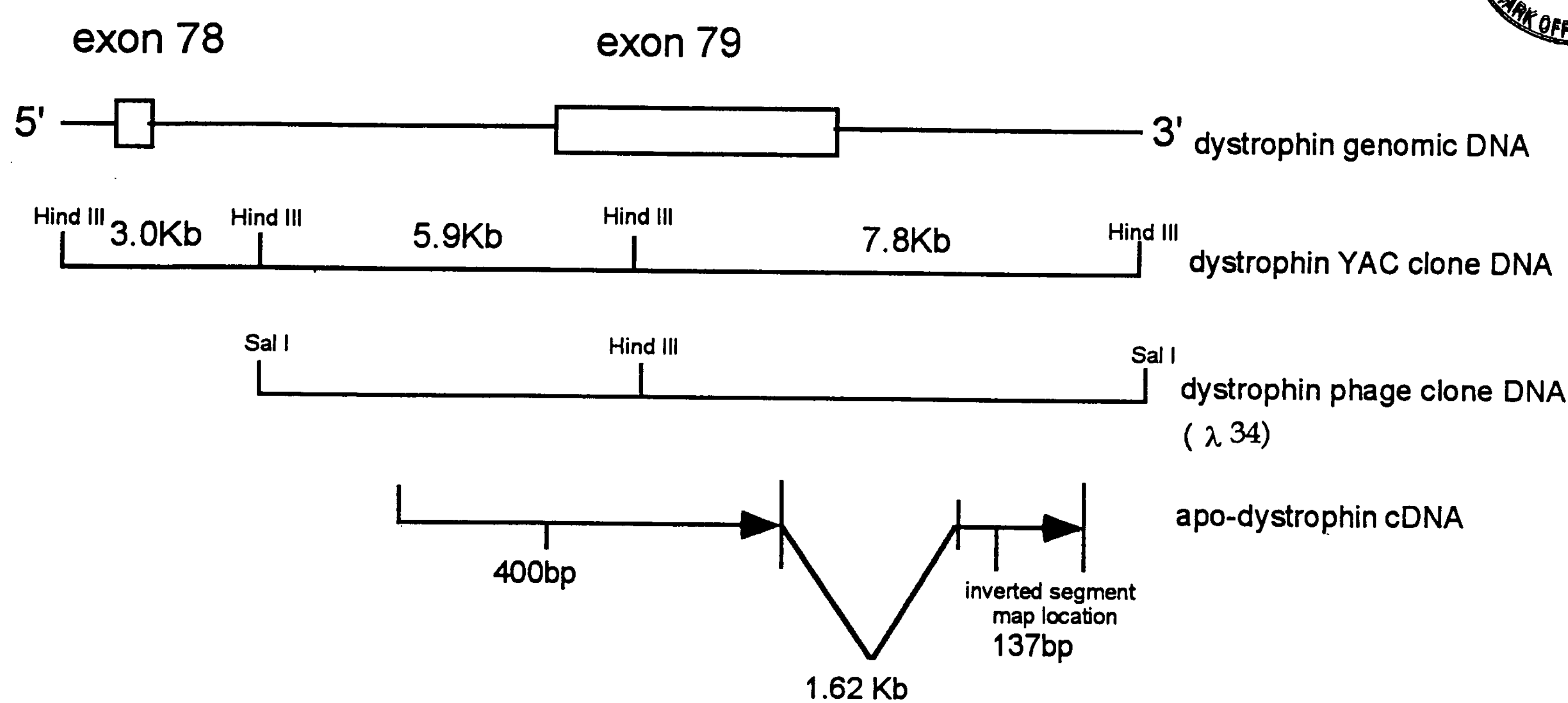

*cDNA map is not precisely drawn to scale

Figure 8

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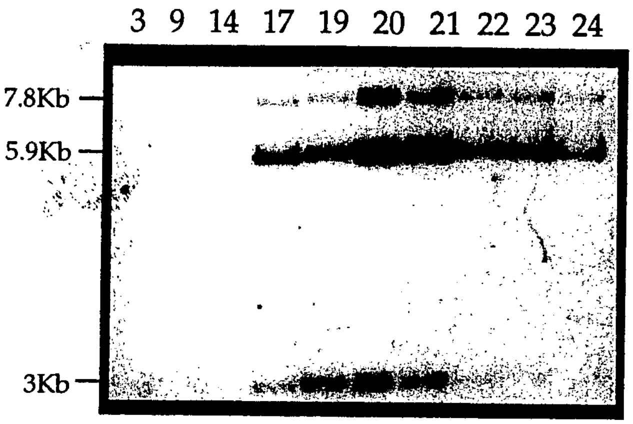
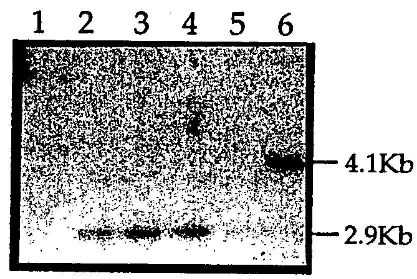


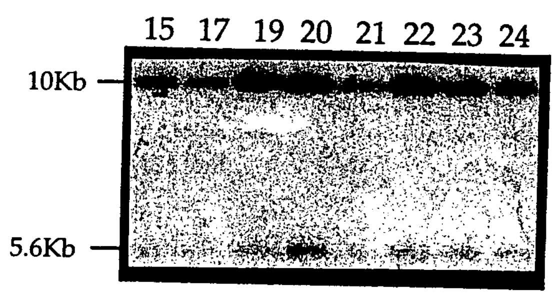
A. Human

Figure 9A



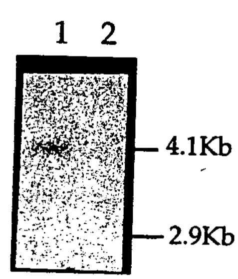
B. Mouse

Figure 9B



A. Human

Figure 10A



B. Mouse

Figure 10B

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```
                             1                                                  50
(SEQ ID NO 54) Mgen1073      .......... .......... .......... .......... ..........
(SEQ ID NO 55) Hapo1234      ctagtttcct attcaatgta tagtgcacca aaggtcaatt caagagttta
             Consensus      ---------- ---------- ---------- ---------- ----------

                             51                                                 100
               Mgen1073      .......... .......... .......... .......... ..........
               Hapo1234      ttattattat tttcaaccca agtaaaagca gagagaaaat agccacctcc
              Consensus      ---------- ---------- ---------- ---------- ----------

                             101                           begin GRAIL exon @149 150
               Mgen1073      .......... .......... ttcACAGgCT tAAgCAGCca gtAAATGAcA
               Hapo1234      accatagcct cagaagcaag ccaACAGcCT gAAaCAGCtt tgAAATGAaA
              Consensus      ---------- ---------- ---ACAG-CT -AA-CAGC-- --AAATGA-A

                             151                                                200
               Mgen1073      AtT....... .......... .........T AtgtGgtAgt cAgGtcactG
               Hapo1234      AgTtggtgtg gcggtgatgg tggcagtgaT AatgGtgAcc gAtGgttggG
              Consensus      A-T------- ---------- ---------T A---G--A-- -A-G-----G

                             201                                   apo-4 5'end 250
               Mgen1073      TGCTGGTaAT GGTgaTctTA GcaGgcAgAG aaGGTGgTaG TGaTTTGATa
               Hapo1234      TGCTGGTgAT GGTagTggTA GttGtgA.AG gtGGTGaTgG TGgTTTGATt
              Consensus      TGCTGGT-AT GGT--T--TA G--G--A-AG --GGTG-T-G TG-TTTGAT-

                             251      M1                                    300
               Mgen1073      GtaAaagtgt AgAcTaTaCa acAgaAtAAa TAcAagtatA GTAA......
               Hapo1234      GatAgtaaaa AaAaTgTtCg ttAatAcAAg TAgAgagtaA GTAAtcaatc
              Consensus      G--A------ A-A-T-T-C- --A--A-AA- TA-A-----A GTAA------

                             301                          M2        M3       350
               Mgen1073      .......atc caaCAAaGTG tgAAAGgTGT gTgCCATtAc acAtctTTCt
               Hapo1234      aatcactcat agcCAAgGTG gaAAAGaTGT aTcCCATcAt ggAataTTCc
              Consensus      ---------- ---CAA-GTG --AAAG-TGT -T-CCAT-A- --A---TTC-

                             351                                                400
               Mgen1073      cG........ GtgATaagag cCTTgTCTAT GaAgTTC... TGAgATgTgT
               Hapo1234      tGttctgata GaaATcttgt gCTTaTCTAT GgAaTTCttt TGAtATaTaT
              Consensus      -G-------- G--AT----- -CTT-TCTAT G-A-TTC--- TGA-AT-T-T

                             401                                                450
               Mgen1073      TaggAagatG AAtCatcAat TtaCaT.... TTcTcCCcat cAAAtgaCAc
               Hapo1234      TtacAttggG AAcCtgaAtg TagCtTgaca TTtTtCCatg tAAAcacCAg
              Consensus      T---A----G AA-C---A-- T--C-T---- TT-T-CC--- -AAA---CA-

                             451              begin mouse GRAIL exon            500
               Mgen1073      cAtgCTGATC CAgtATTAAG CTaATACTAA C.....ACca tgcAatGCTT
               Hapo1234      tAgcCTGATC CAacATTAAG CTgATACTAA CaaacaACgt gtaAtgGCTT
              Consensus      -A--CTGATC CA--ATTAAG CT-ATACTAA C-----AC-- ---A--GCTT

                             501                                                550
               Mgen1073      CATTAAcAAG GaTTTGCTTC TTgCTaGAAA tgGGT..AAA AaCggACtgT
               Hapo1234      CATTAAtAAG GcTTTGCTTC TTcCTgGAAA ctGGTgaAAA AtCaaACctT
              Consensus      CATTAA-AAG G-TTTGCTTC TT-CT-GAAA --GGT--AAA A-C--AC--T
```

Figure 11

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-70 bp from 5' end of apo-4

```
  Inr = GCCC TCAT TCTG GAGAC   (SEQ ID NO: 59)
apo-4 = GCGG TGAT GGTG GCAGT   (SEQ ID NO: 60)
```

- 48% perfect homology with Inr

71% match on type of base

(purine vs. pyrimidine)

Figure 12B

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```
           551                                                600
Mgen1073   GgTcTGTAtA CCtTCaATGC AGCTTaTGTG TTGTCTTttC C..tgAAatG
Hapo1234   GtTgTGTAcA CCcTCgATGC AGCTTcTGTG TTGTCTTcaC CcagaAAtgG
Consensus  G-T-TGTA-A CC-TC-ATGC AGCTT-TGTG TTGTCTT--C C----AA--G

           601                                                650
Mgen1073   GtAATGAcTc CCaAtAgtGg cAAccAgggG tacaATaCT. ......TGCA
Hapo1234   GgAATGAtTt CCcAaAtgGc aAAgaAacaG agtgATgCTa tctatcTGCA
Consensus  G-AATGA-T- CC-A-A--G- -AA--A---G ----AT-CT- ------TGCA


           651                                        exon79 700
Mgen1073   CacTTTGTAA A....cTCTT TCTTTCTCTT TGTTTTCCAG GACACAATGT
Hapo1234   CctTTTGTAA AgtctgTCTT TCTTTCTCTT TGTTTTCCAG GACACAATGT
Consensus  C--TTTGTAA A-----TCTT TCTTTCTCTT TGTTTTCCAG GACACAATGT

           701                                                750
Mgen1073   AGGAAGcCTT TTCCACATGG CAGATGATTT GGGCAGAGCG ATGGAGTCCT
Hapo1234   AGGAAGtCTT TTCCACATGG CAGATGATTT GGGCAGAGCG ATGGAGTCCT
Consensus  AGGAAG-CTT TTCCACATGG CAGATGATTT GGGCAGAGCG ATGGAGTCCT

           751                                                800
Mgen1073   TAGTtTCAGT CATGACAGAT GAAGAAGGAG CAGAATAAAT GTTTTACAAC
Hapo1234   TAGTaTCAGT CATGACAGAT GAAGAAGGAG CAGAATAAAT GTTTTACAAC
Consensus  TAGT-TCAGT CATGACAGAT GAAGAAGGAG CAGAATAAAT GTTTTACAAC

           801                                                850
Mgen1073   TCCTGATTCC CGCATGGTTT TTATAATATT CgTACAACAA AGAGGATTAG
Hapo1234   TCCTGATTCC CGCATGGTTT TTATAATATT CaTACAACAA AGAGGATTAG
Consensus  TCCTGATTCC CGCATGGTTT TTATAATATT C-TACAACAA AGAGGATTAG

           851                                                900
Mgen1073   ACAGTAAGAG TTTACAAGAA ATaAAATCTA TATTTTTGTG AAGGGTAGTG
Hapo1234   ACAGTAAGAG TTTACAAGAA AT.AAATCTA TATTTTTGTG AAGGGTAGTG
Consensus  ACAGTAAGAG TTTACAAGAA AT-AAATCTA TATTTTTGTG AAGGGTAGTG

           901                                                950
Mgen1073   GTAcTATACT GTAGATTTCA GTAGTTTCTA AGTCTGTTAT TGTTTTGTTA
Hapo1234   GTAtTATACT GTAGATTTCA GTAGTTTCTA AGTCTGTTAT TGTTTTGTTA
Consensus  GTA-TATACT GTAGATTTCA GTAGTTTCTA AGTCTGTTAT TGTTTTGTTA

           951                                               1000
Mgen1073   ACAATGGCAG GTTTTACACG TCTATGCAAT TGTACAAAAA AGTTAaAAGA
Hapo1234   ACAATGGCAG GTTTTACACG TCTATGCAAT TGTACAAAAA AGTTAtAAGA
Consensus  ACAATGGCAG GTTTTACACG TCTATGCAAT TGTACAAAAA AGTTA-AAGA

           1001                                              1050
Mgen1073   AA...ACATG TAAAATCTTG ATAGCTAAAT AACTTGCCAT TTCTTTATAT
Hapo1234   AAactACATG TAAAATCTTG ATAGCTAAAT AACTTGCCAT TTCTTTATAT
Consensus  AA---ACATG TAAAATCTTG ATAGCTAAAT AACTTGCCAT TTCTTTATAT
```

Figure 11 (cont'd)

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```
                                               begin inversion@1100
           1051                                                   1100
  Mgen1073 GGAACGCATT TTGGGTTGTT TAAAAATTTA TAACAGTTAT AAAGAAAGAt
  Hapo1234 GGAACGCATT TTGGGTTGTT TAAAAATTTA TAACAGTTAT AAAGAAAGAa
 Consensus GGAACGCATT TTGGGTTGTT TAAAAATTTA TAACAGTTAT AAAGAAAGA-

           1101                                                   1150
  Mgen1073 TgtaAActaA Agtgtgcttt AtAAAAaAAg ttgtTtataA AaacccctAa
  Hapo1234 TtatAAaggA A.......aa AgAAAAtAAc gcaaTggacA AgtggtgaAg
 Consensus T---AA---A A--------- A-AAAA-AA- ----T----A A-------A-

           1151                                                   1200
  Mgen1073 acaaacACaC AcGcacaCAC AcacAcacac AcacaCaCAc AcaCAcAcTG
  Hapo1234 ctgtgaACtC AgGtgtgCAC AattAtcagg AacacCcCAa AacCAaAgTG
 Consensus ------AC-C A-G----CAC A---A----- A----C-CA- A--CA-A-TG

           1201                                        1243
  Mgen1073 AGGcAGcAca ttgtTttGcA ttacTtTagc gTGTatcaTA t..
  Hapo1234 AGGtAGaAat agcaTgaGaA gccgTgTttg aTGTtaatTA att
 Consensus AGG-AG-A-- ----T--G-A ----T-T--- -TGT----TA ---
```

Figure 11 (cont'd)

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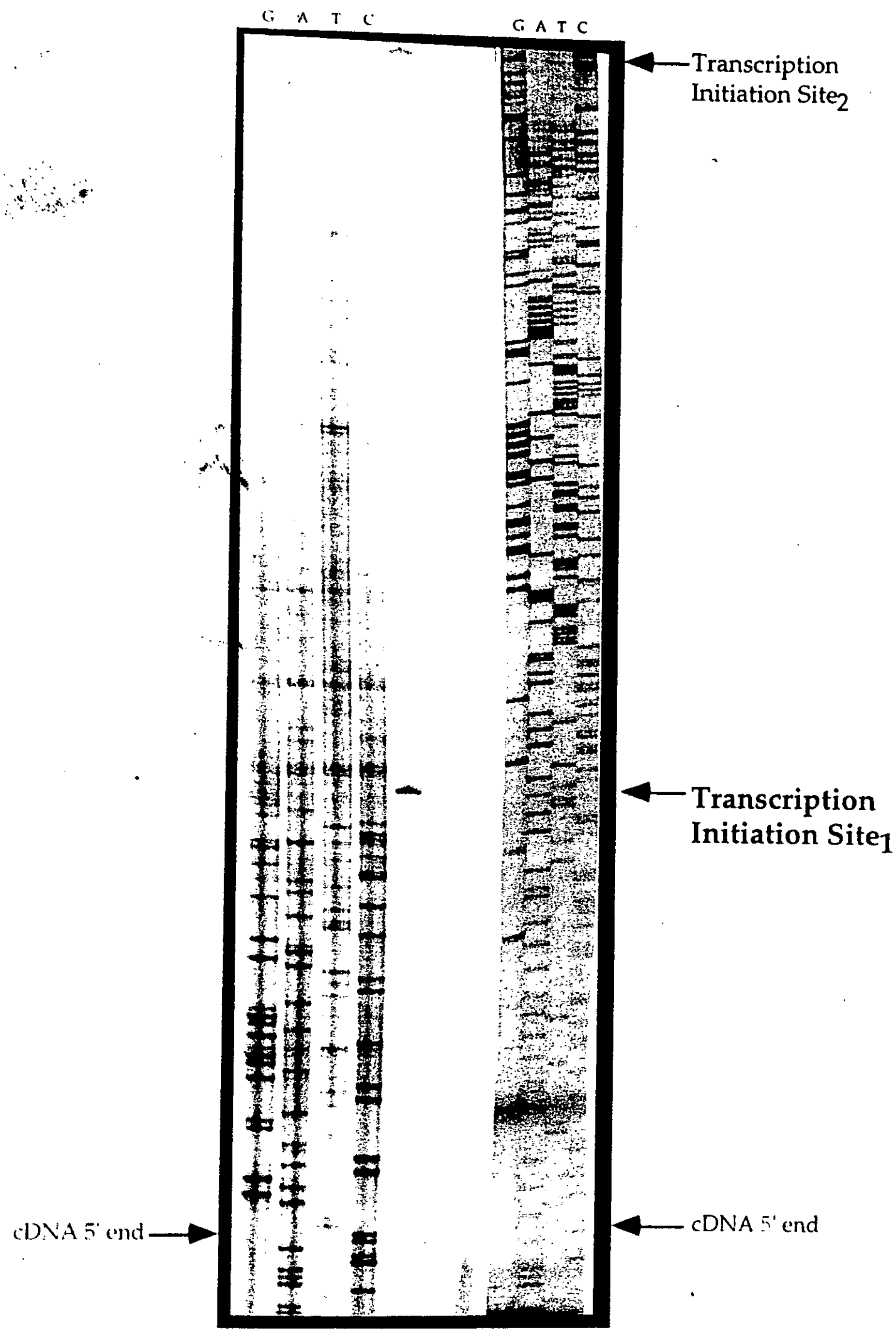

Figure 12A

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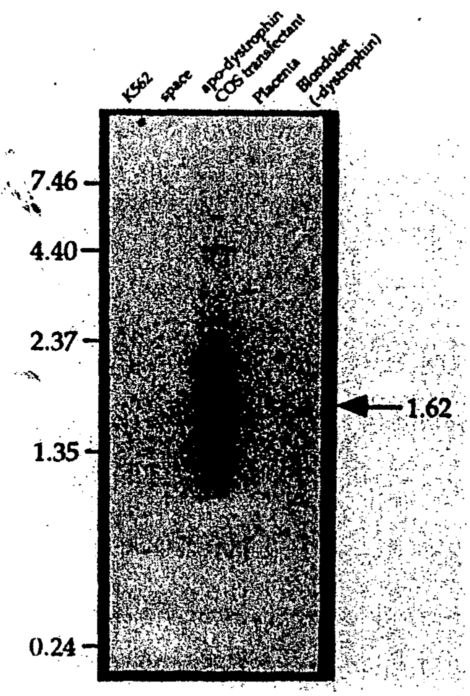

Figure 13

OIPE JC132
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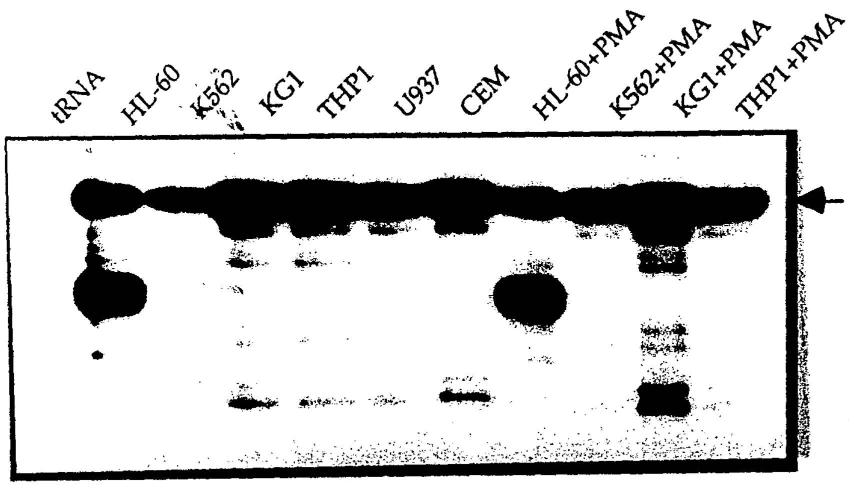

Figure 14

OIPE JC132
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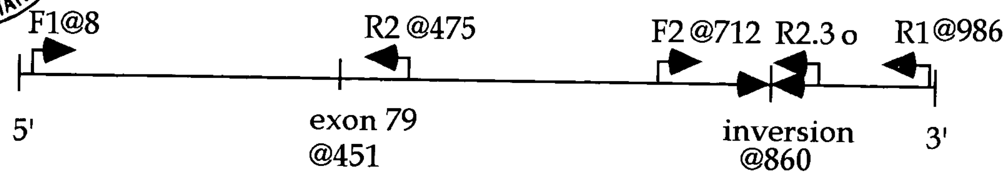
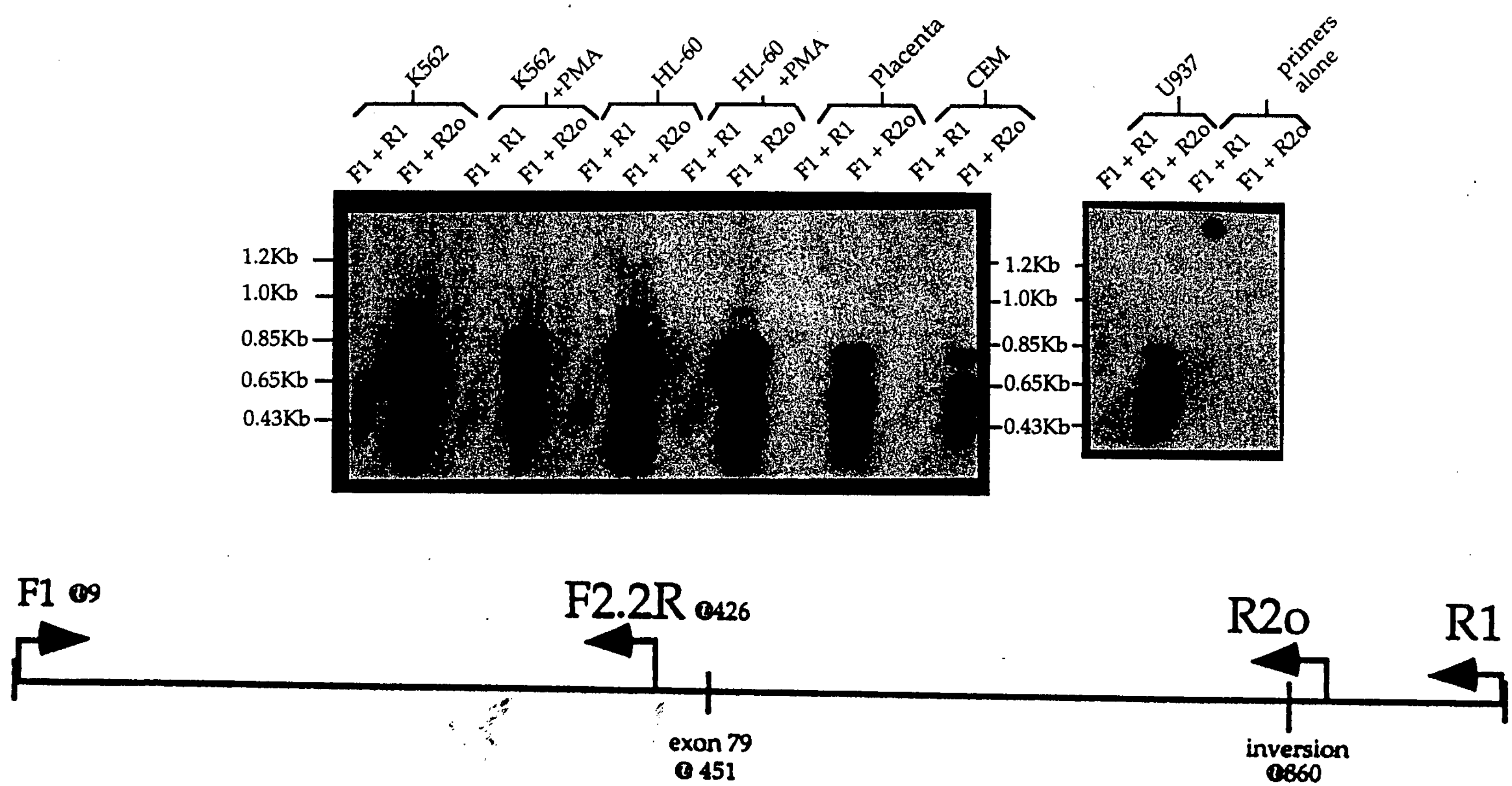


Figure 15



The Apo-dystrophin cDNA

Figure 16

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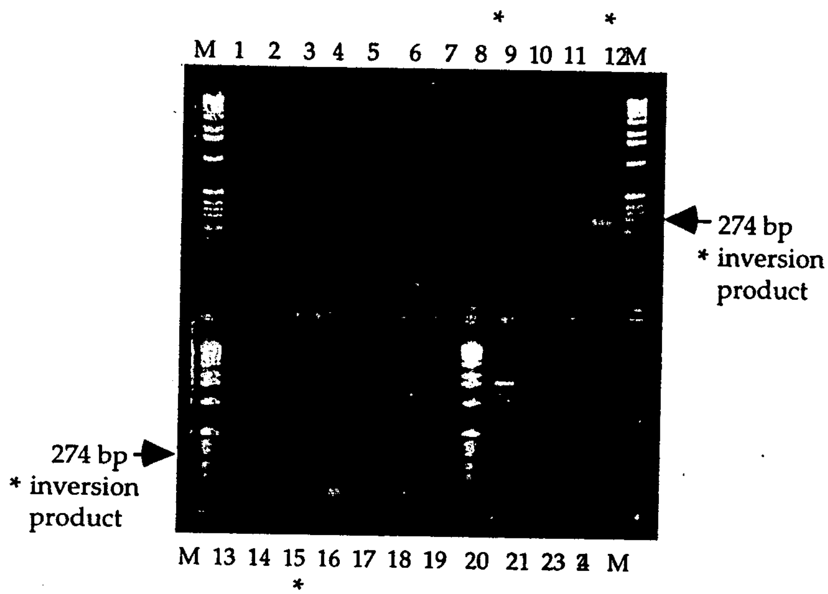
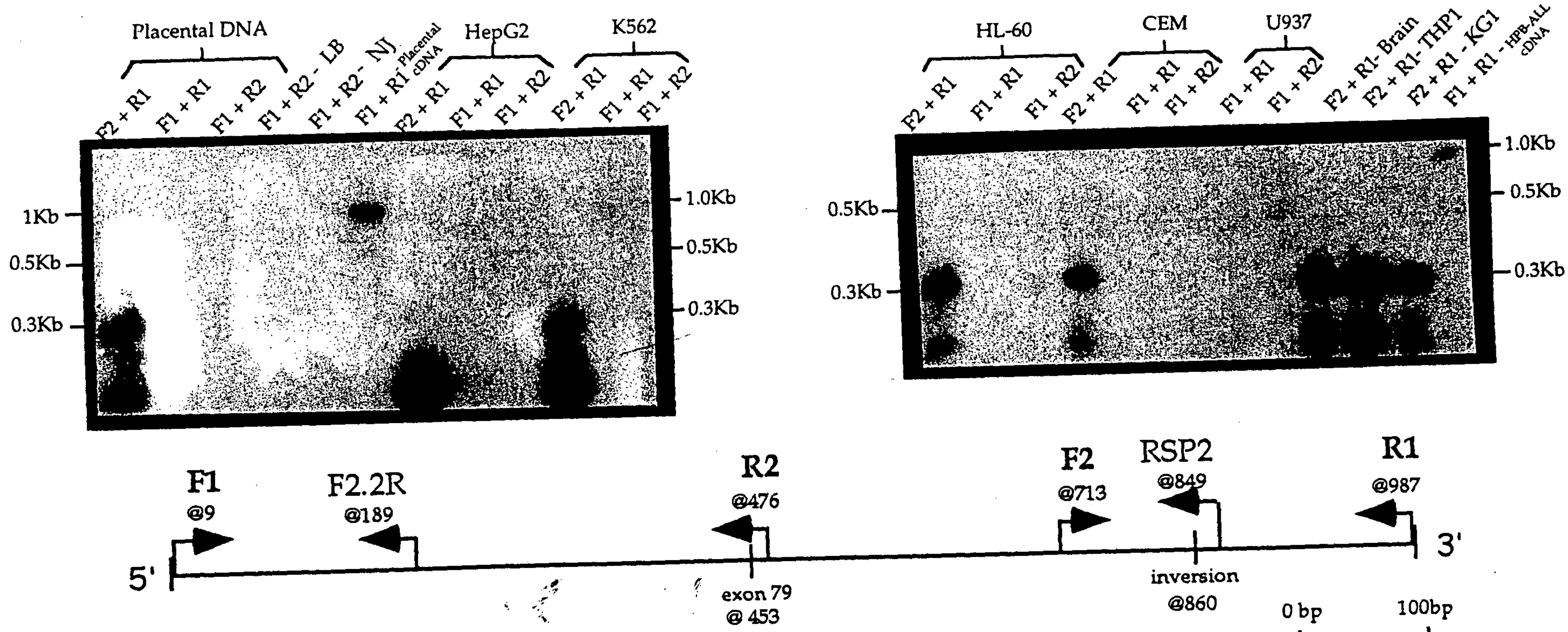


Figure 17A



The Apo-dystrophin cDNA*

*RT-PCR primers (bold) and Southern Blotting probes are indicated by the arrows.

Figure 17B

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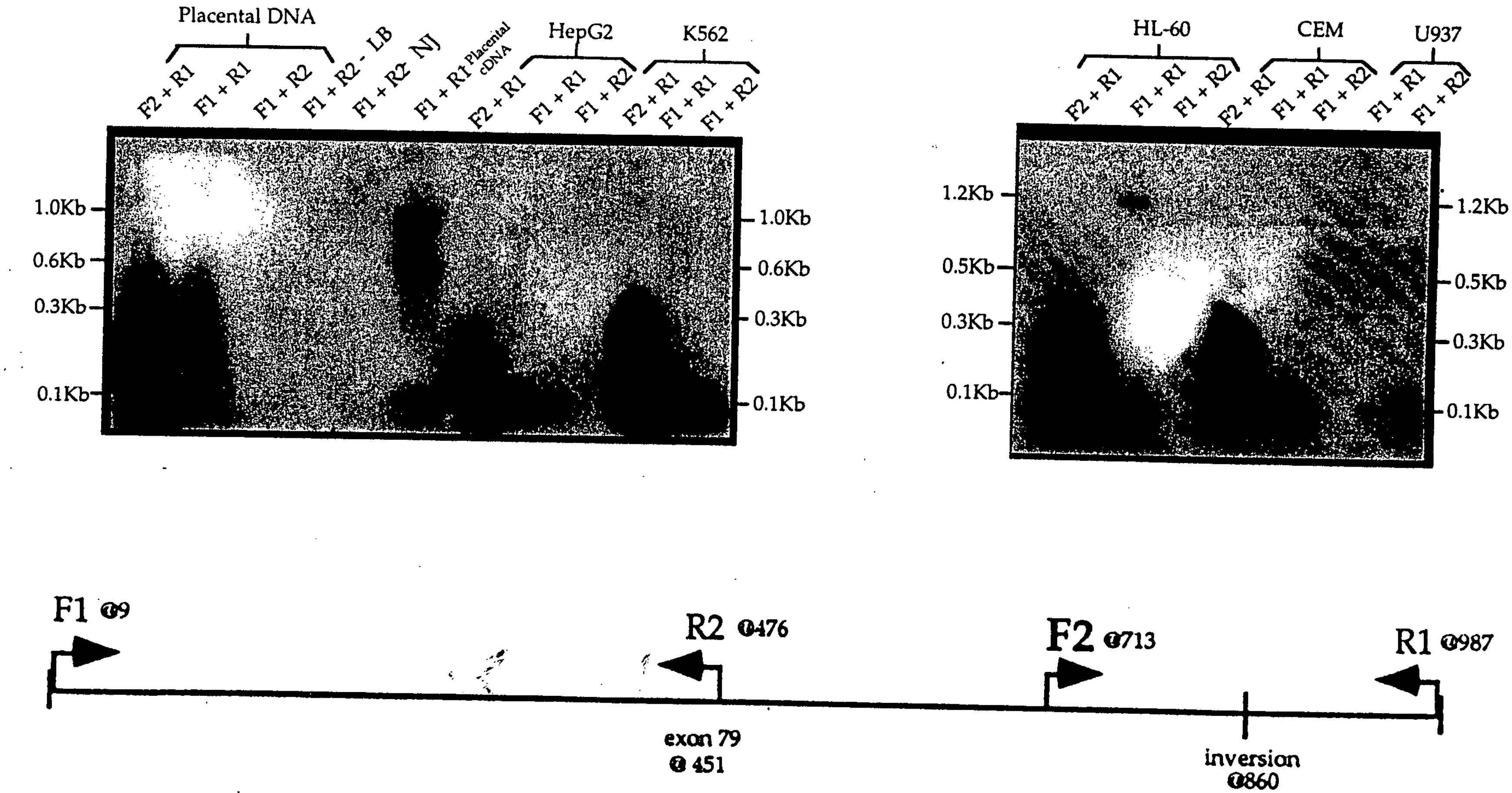

The Apo-dystrophin cDNA

Figure 17C

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A.

```
          12/23bp spacer
CACAGTG-----------------------ACAAAAACC
heptamer                       nonamer
```

Figure 18A

B.

```
                                  inversion breakpoint1
       11640      11650      11660    |  11670      11680
          *          *          *     |     *          *
dystrophin  T TTATAACAGT TATAAAGAAA GA^TTGTAAAC TAAAGTGTGC
            A AATATTGTCA ATATTTCTTT CT^AACATTTG ATTTCACACG
                                      a
apo-4 cDNA   840        850           |        870
[  138 ]    T TTATAACAGT TATAAAGAAA GA^TTaTAAAg gAAAaaGaaa>
            ^ ^^^^^^^^^^ ^^^^^^^^^^ ^^ ^^v^^^^v v^^^vv^vvv
dystrophin  T TTATAACAGT TATAAAGAAA GA^TTGTAAAC TAAAGTGTGC

-------------------------------------------------------------------

                 11690      11700      11710      11720      11730
                     *          *          *          *          *
dystrophin  TTTATAAAAA AAAGTTGTTT ATAAAAACCC CTAAAAACAA AACAAACACA
            AAATATTTTT TTTCAACAAA TATTTTTGGG GATTTTTGTT TTGTTTGTGT
apo-4 cDNA   880    890         900        910        920        930
[  138 ]    aTaAaAtggA cAAGTgGTga ATgtgAACtC aggtgtgCAc AAttAtCAgg>
            v^v^v^vvv^ v^^^^v^^vv ^^vvv^^^v^ vvvvvvv^^v ^^vv^v^^vv
dystrophin  TTTATAAAAA AAAGTTGTTT ATAAAAACCC CTAAAAACAA AACAAACACA

-------------------------------------------------------------------

                 11740      11750
                     *          *
dystrophin  CACACACACA CATACACACA
            GTGTGTGTGT GTATGTGTGT
apo-4 cDNA    940        950
[  138 ]    aACAC-CcCA -AaAC-CAaA>
            v^^^^ ^v^^  ^v^^ ^^v^
dystrophin  CACACACACA CATACACACA
```

Figure 18B (SEQ ID NO: 57)

OIPE JC132
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```
                                                          inversion breakpoint2
                13130       13140       13150       13160   |   13170
                    *           *           *           *   |       *
dystrophin  AATTAGCTTT TGGAGAGTGG GTTTTGTCCA TTATTAATAA  TTAATTAATT
            TTAATCGAAA ACCTCTCACC CAAAACAGGT AATAATTATT  AATTAATTAA

                                                                  990
apo-4       ____________________________________________<AATTAATT
                                                          ^^^^^^^^
dystrophin                                                AATTAATT

-------------------------------------------------------------------
                 13180       13190       13200       13210       13220
                     *           *           *           *           *
dystrophin   AACATCAAAC ACGGCTTCTC ATGCTATTTC TACCTCACTT TGGTTTTGGG
             TTGTAGTTTG TGCCGAAGAG TACGATAAAG ATGGAGTGAA ACCAAAACCC

                   980         970         960         950         940
apo-4       <AACATCAAAC ACGGCTTCTC ATGCTATTTC TACCTCACTT TGGTTTTGGG
             ^^^^^^^^^^ ^^^^^^^^^^ ^^^^^^^^^^ ^^^^^^^^^^ ^^^^^^^^^^
dystrophin   AACATCAAAC ACGGCTTCTC ATGCTATTTC TACCTCACTT TGGTTTTGGG

-------------------------------------------------------------------
                 13230       13240       13250       13260       13270
                     *           *           *           *           *
dystrophin   GTGTTCCTGA TAATTGTGCA CACCTGAGTT CACAGCTTCA CCACTTGTCC
             CACAAGGACT ATTAACACGT GTGGACTCAA GTGTCGAAGT GGTGAACAGG

                   930         920         910         900         890
apo-4       <GTGTTCCTGA TAATTGTGCA CACCTGAGTT CACAGCTTCA CCACTTGTCC
             ^^^^^^^^^^ ^^^^^^^^^^ ^^^^^^^^^^ ^^^^^^^^^^ ^^^^^^^^^^
dystrophin   GTGTTCCTGA TAATTGTGCA CACCTGAGTT CACAGCTTCA CCACTTGTCC

-------------------------------------------------------------------
                 13280       13290       13300       13310       13320
                     *           *           *           *           *
dystrophin   ATTGCGTTAT TTTCTTTTTC CTTTATAATT CTTTCTTTTT CCTTCATAAT
             TAACGCAATA AAAGAAAAAG GAAATATTAA GAAAGAAAAA GGAAGTATTA
                                             |
                              inversion breakpoint3
                   880         870         860         850         840
apo-4       <ATTGCGTTAT TTTCTTTTTC CTTTATAATT CTTTCTTTaT aacTgtTAta
             ^^^^^^^^^^ ^^^^^^^^^^ ^^^^^^^^^^ ^^^^^^^^v^ vvv^vv^^vv
dystrophin   ATTGCGTTAT TTTCTTTTTC CTTTATAATT CTTTCTTTTT CCTTCATAAT
```

Figure 18C (SEQ ID NO: 58)

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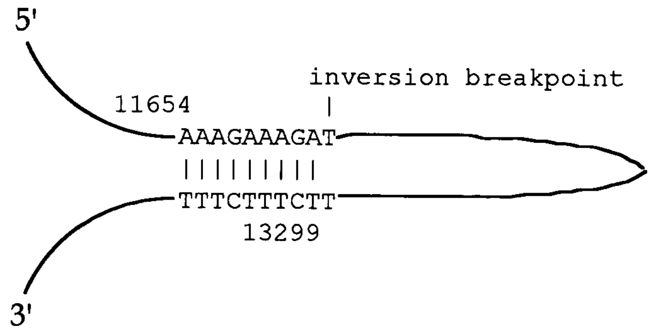
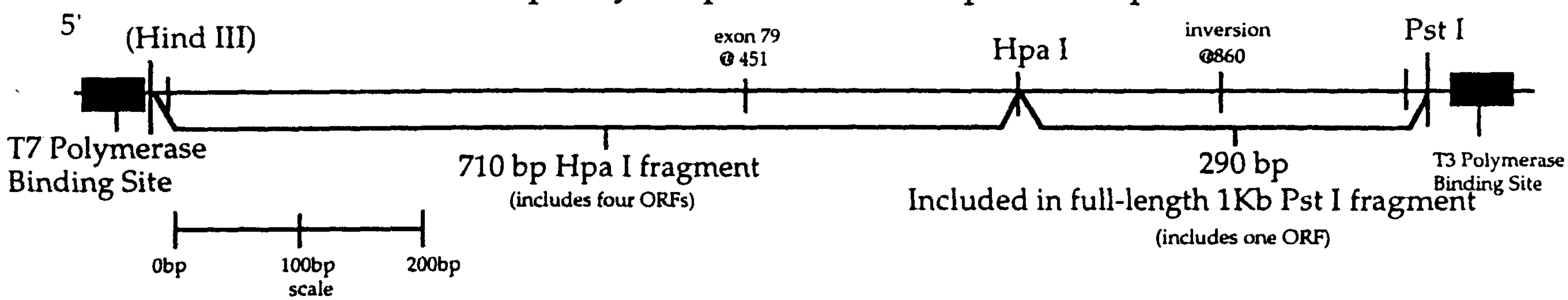


Figure 18D (Sequence included in SEQ ID NO: 57)

```
                      inversion @ 860
    TAACAGTTATAAAGAAAGAATTATAAAGGAAAAAGAAAATAACGCAATGGACAAGTGGTG
841 ---------+---------+---------+---------+---------+---------+ 900
    ATTGTCAATATTTCTTTCTTAATATTTCCTTTTTCTTTTATTGCGTTACCTGTTCACCAC
```

Figure 19 (Sequence included in SEQ ID NO: 2)

Description of *In Vitro* Transcription and Translation of the Apo-dystrophin cDNA in pBluescript SK+



Linearize plasmid with either HpaI (truncated) or Pst I (full length). Gene Clean and incubate with T7 polymerase and dNTPs to produce RNA in vitro.

↓

Incubate RNA with Wheat Germ Extract or Rabbit Reticulocyte Lysates to produce *in vitro* translation

↓

Separate translation products by SDS-PAGE. Fix, Amplify and Dry Gel. Perform Autoradiography

Figure 20

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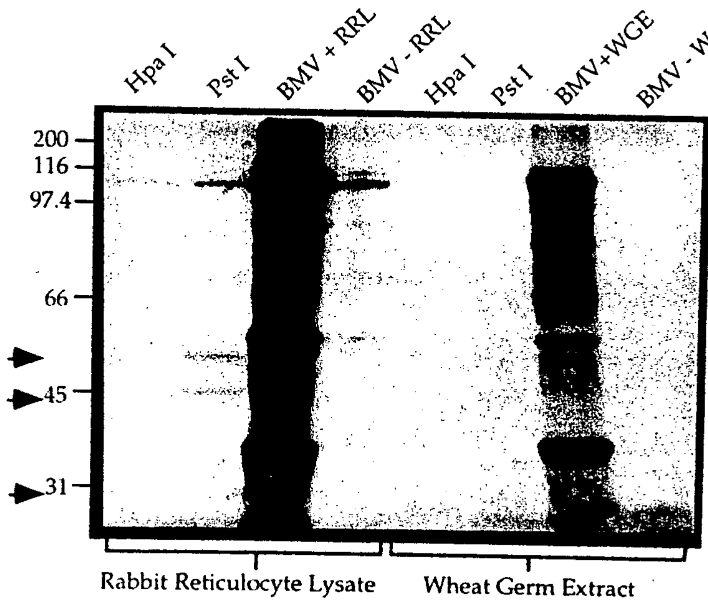

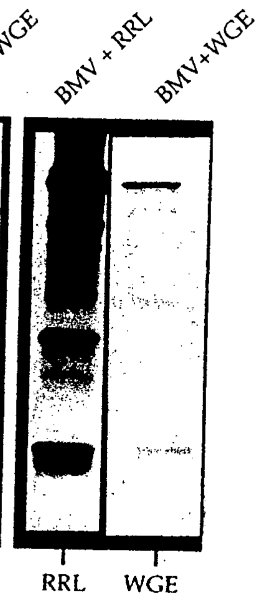

Figure 20A **Figure 20B**

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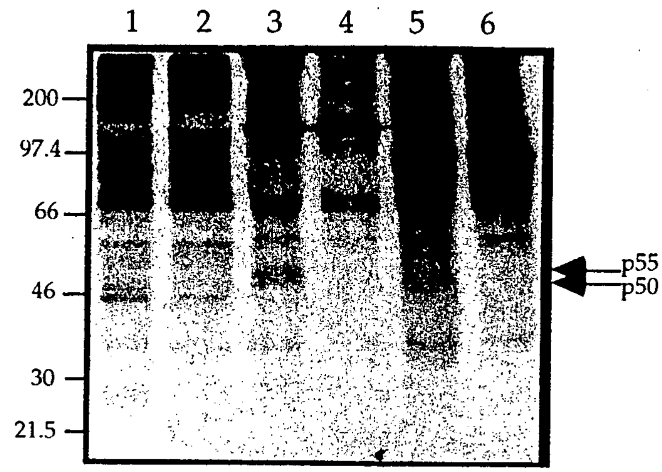

Figure 21

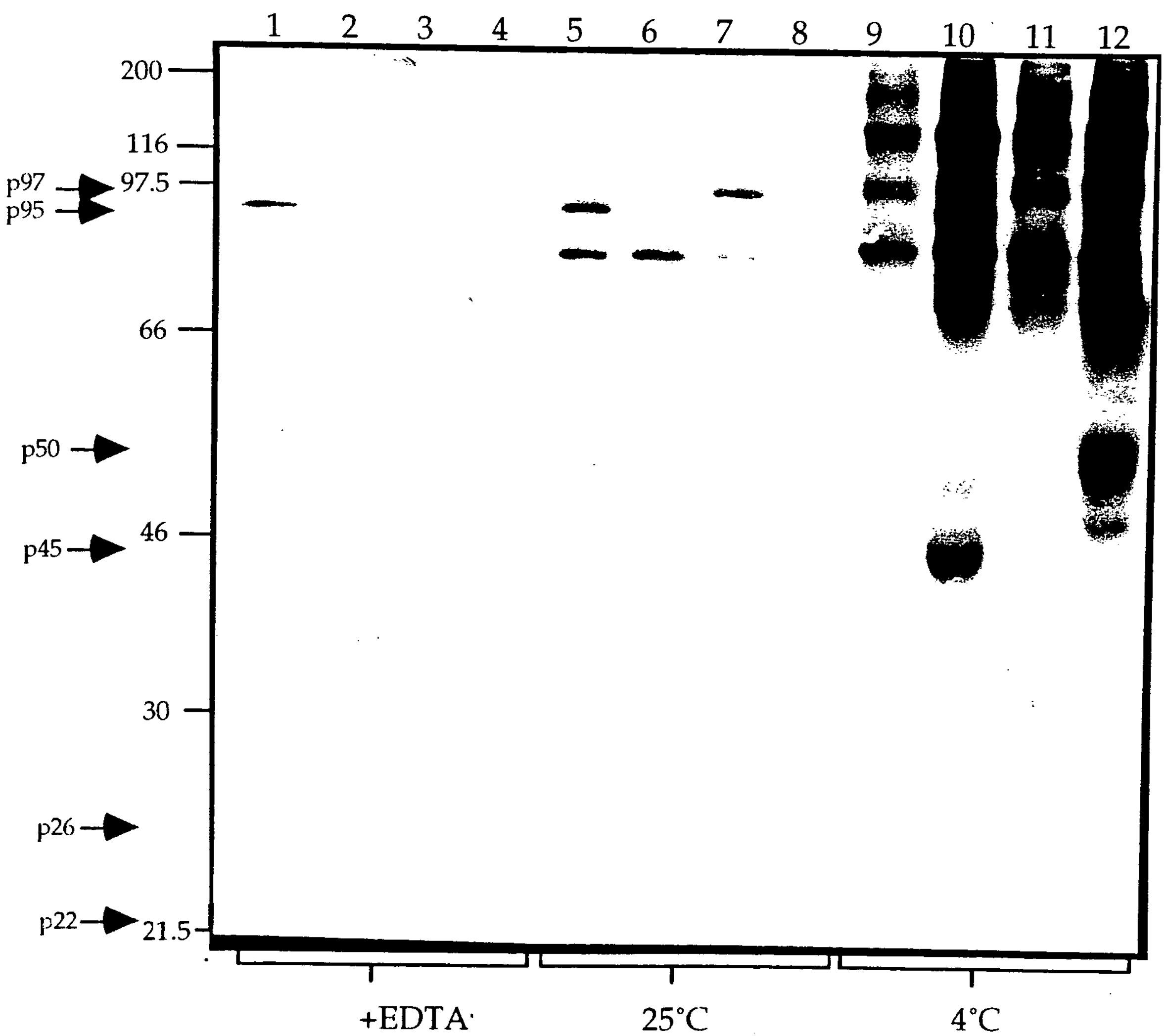

Figure 22

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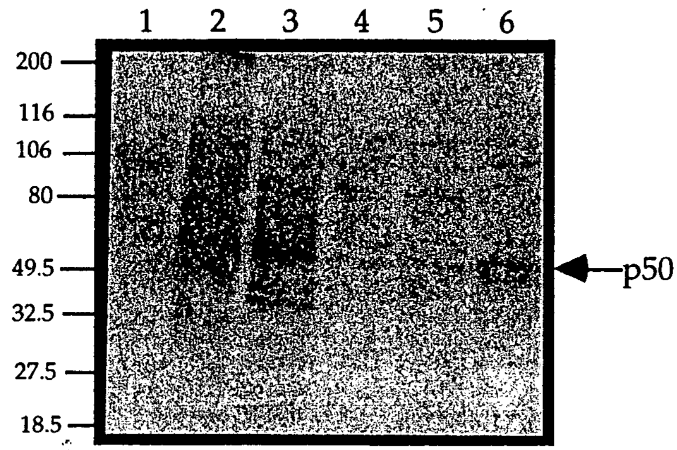

Figure 23

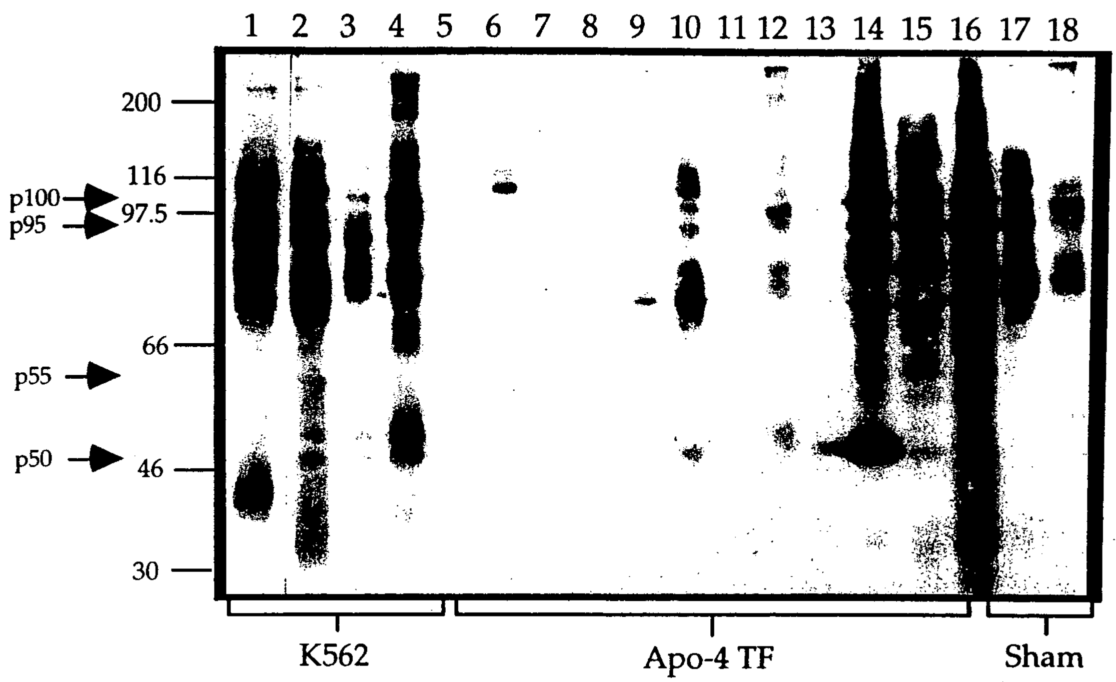

Figure 24

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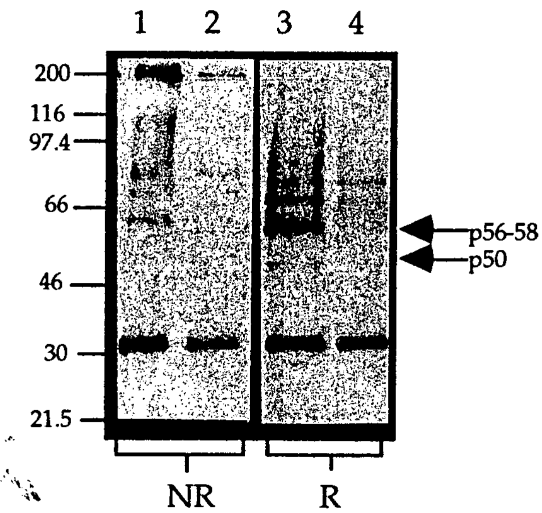

Figure 25A

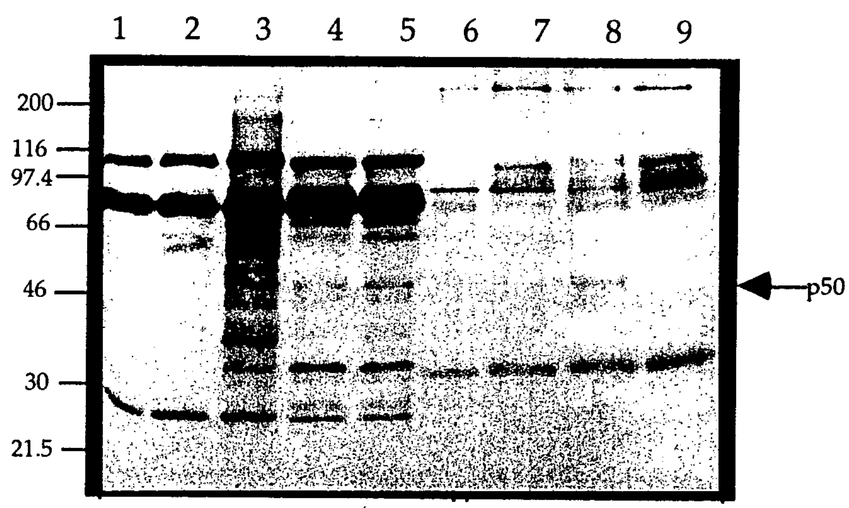

Figure 25B

H2 starting at second methionine - 321 bp, predicted weight = 17.4Kd + 1 N-glycosplation site + 20.4 Kd.

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Figure 26A

Splice sites for peptide

MYPIMEYSCSDRNLVLIYGILLIYIYIGNLNMKKEQNKCFTTPDSRMVFIIFI
QQRGLDSKSLQEINLYFCEGFYTSMQLYKKVIRKLHKITQWTRTPQNQSEV
EIA (SEQ ID NO: 61)

Figure 26B

Start	Exon No.	Exon Position	Exon Length	Intron No.	Intron Position	Intron Length
@88 bp	78.3	@74-180	106 bp	79.1	@181-529	349 bp
	79.1	@530-654	125 bp	79.4	@655-720	66 bp
	79.4	@721-769	49 bp	79.55	@770-875	105 bp
	79.55	@876-893	18 bp	79.75	@894-932	39 bp
	79.85	@933-966	33 bp			

Hydrophobicity Scale KD; Candidate membrane-spanning segments:

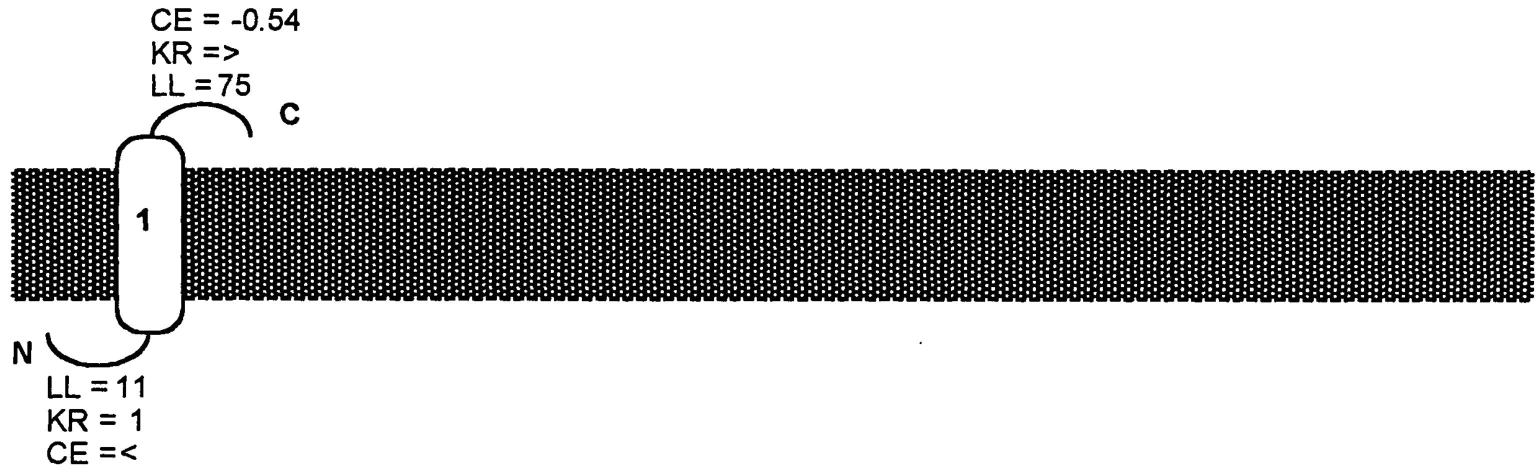
Certain 1 12- 32 1.8833

Figure 26C

Predicted TM structure

> : Too long to be significative
< : Too short to be significative
Ll : Loop length
KR : Number of Lys and Arg

KR Diff : Positive charge difference
CE : Net charge energy
CE Diff : Net charge difference
CH Diff : Charge difference over N-term segments



KR Diff = 1 **CYTOPLASM**
CH Diff = -3 **OUTSIDE**
CE Diff = 0.54 **OUTSIDE**

Structure no. 1

Figure 26D

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A readthrough apo-4S product using the second available methionine

The Apo-4S peptide sequence

P1 Begin TM1(R)
+30 | P2
MYPIMEYSCSD RNLVLIYGIL LIYIYIGNLN V**AR**HFSM**K**TP
VA**R**SNIKLIL 80

TNNV**K**WLH**KK** GFASSWKLVK NQTLLCTPSM QLLCCLHPEM
GNDFPNGKET 130

P3
E**R**CYLSAPFV KSVFLSLCFP GHNVGSLFHM A**DDLGRAMES**
LVSVMTDEEG **180**

AE**K**MFYNS**R**F PHGFYNIHTT KRIRQ**K**EFTR NKSIFL**R**RVV VLYCRFQ**K**FL
230

SLLLFC**K**QWQ VLHVYAIVQK SYKKTTCKIL IAK**K**LAISLY
GTHFGLFKNL 280

KQL**K**RKNYKG KRK**K**RNGQVV KL**R**TQVCTII RNTPKPK**R**GR
NSMRSRV**RCK** 330

LI 332 (302aa in predicted polypeptide) (SEQ ID NO: 56)

Figure 27A

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Candidate membrane-spanning segments:

Certain	1	41-61	1.9073
Putative	2	101-121	0.8052
Certain	3	132-152	1.2552
Putative	4	217-237	1.1833
Putative	5	254-274	0.9240

Transmembrane segments included in structure No. 8: 1 2 3 4 5

Loop lengths: 11 39 10 64 16 58; K+R profile: 1 2 5 (9 >22)

K+R difference: -23: -> Orientation: **N-out**

Charge-difference over N-terminal Membr. segs. (±15 residues): -4
-> Orientation: **N-out**

CYT-EXT profile (neg. values indicate cytoplasmic preference): < -0.13 <

CYT-EXT difference: 0.13: -> Orientation: **N-out**

Figure 27B

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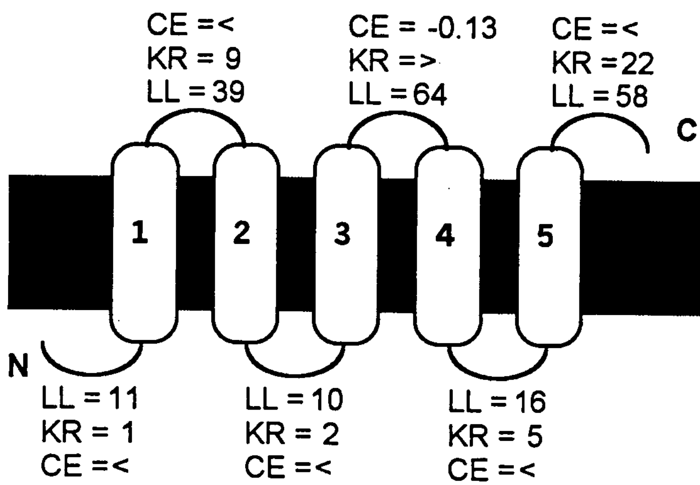
> : Too long to be significative
< : Too short to be significative
LI : Loop length
KR : Number of Lys and Arg

KR Diff : Positive charge difference
CE : Net charge energy
CE Diff : Net charge difference
CH Diff : Charge difference over N-term segments



KR Diff = -23 **OUTSIDE**
CH Diff = -4 **OUTSIDE**
CE Diff = 0.13 **OUTSIDE**

Structure no. 8

Figure 27C

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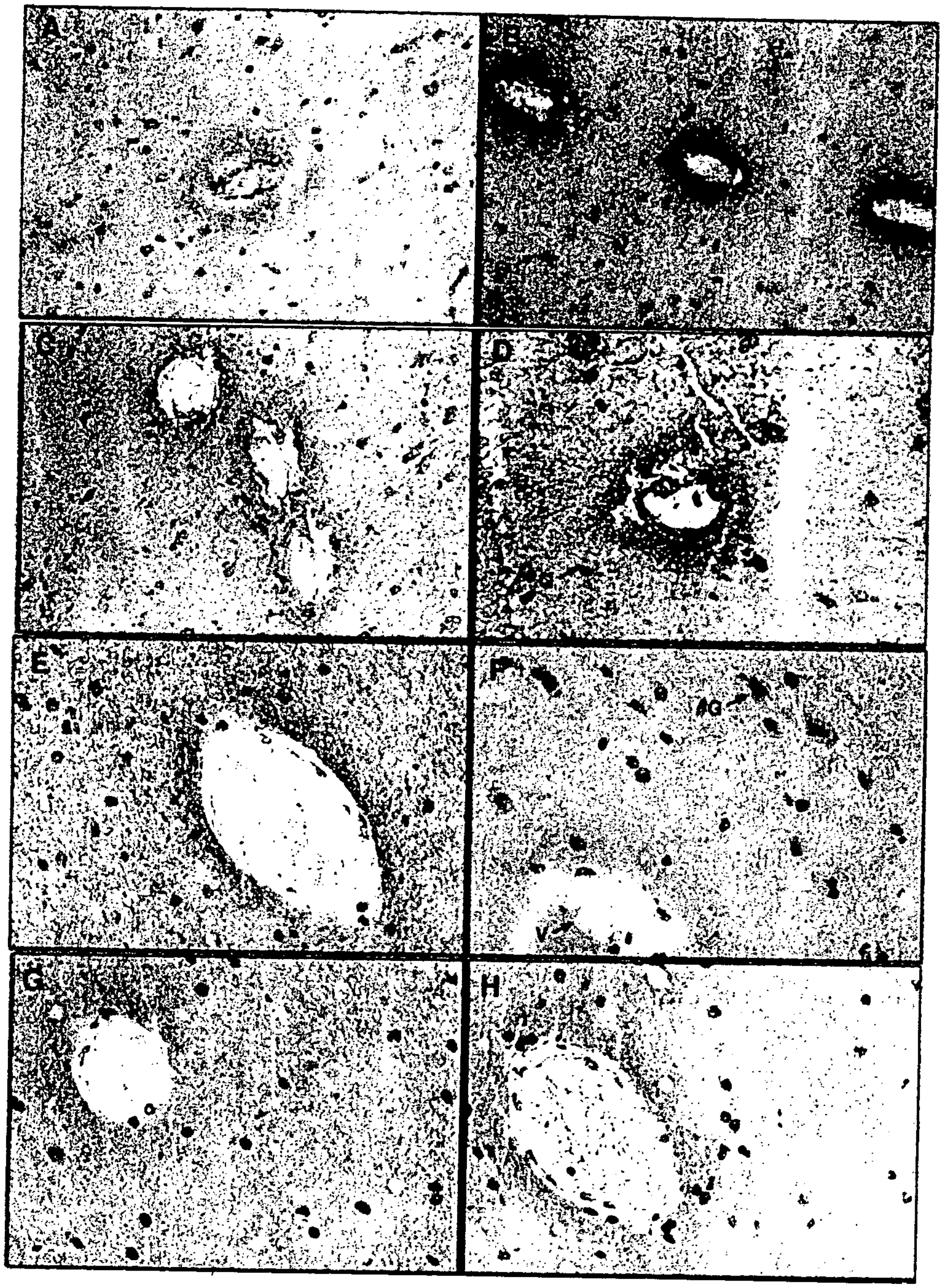

Figure 28

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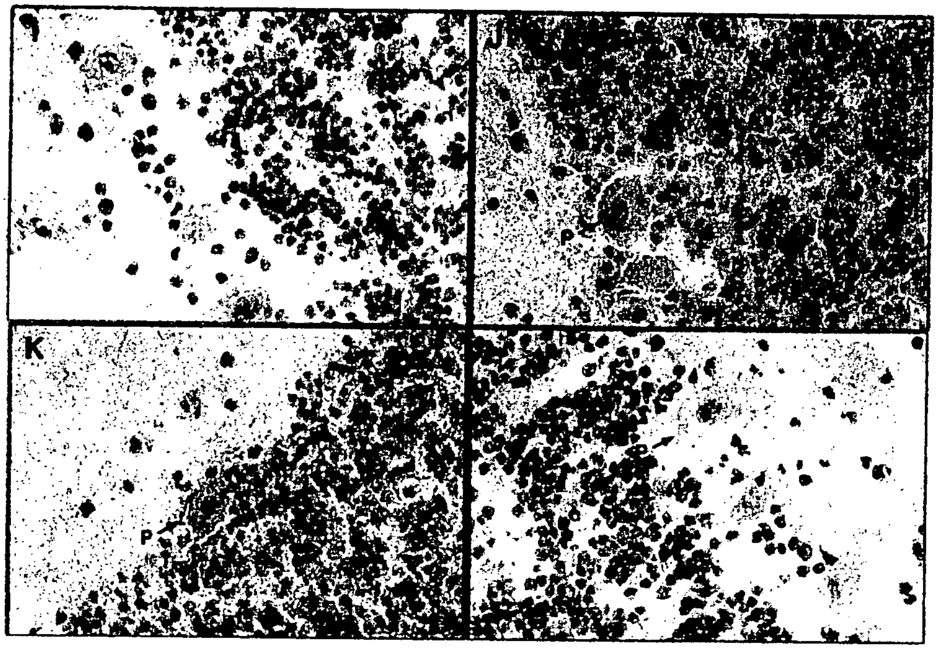

Figure 28 (cont'd)

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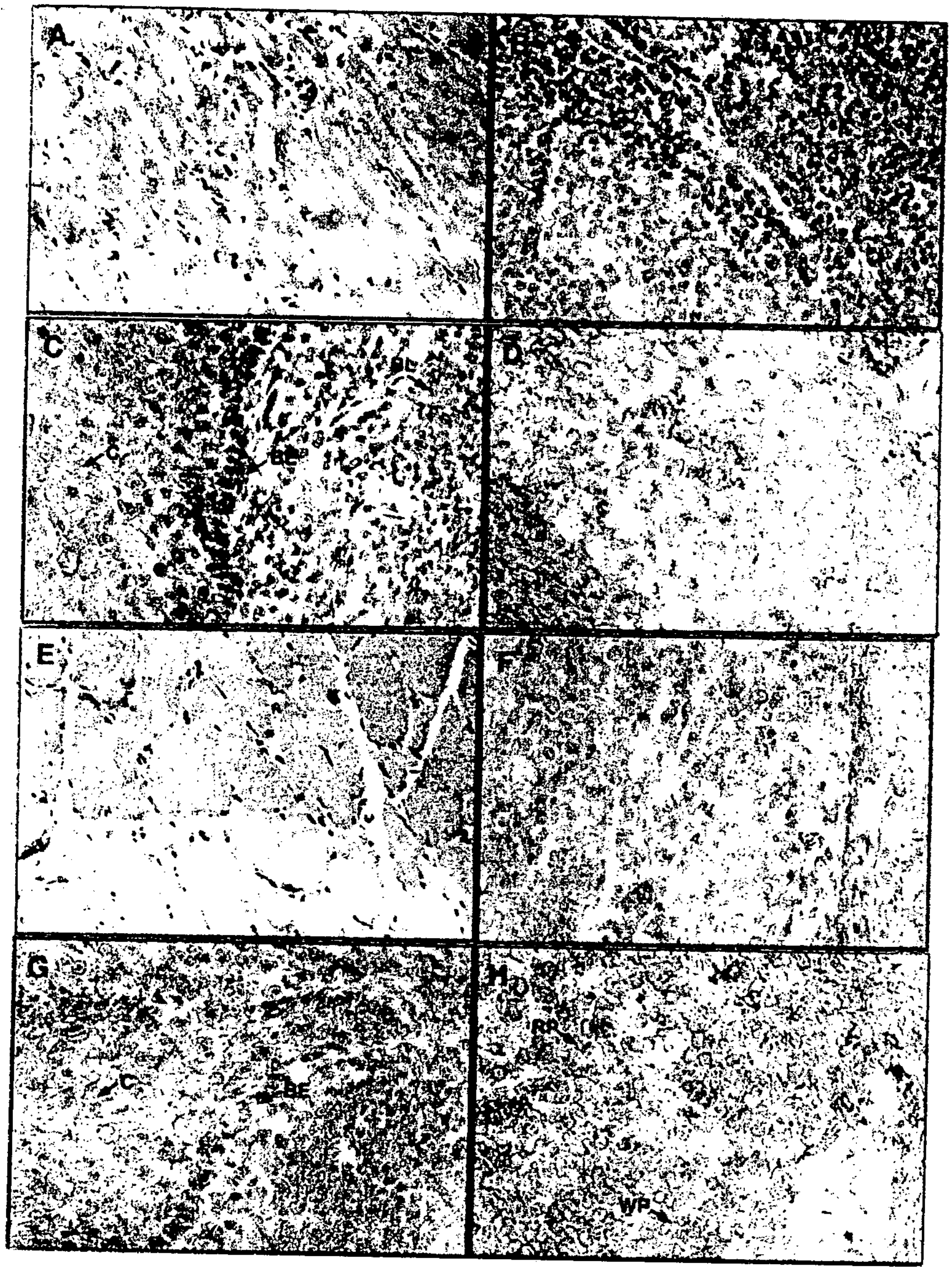

Figure 29

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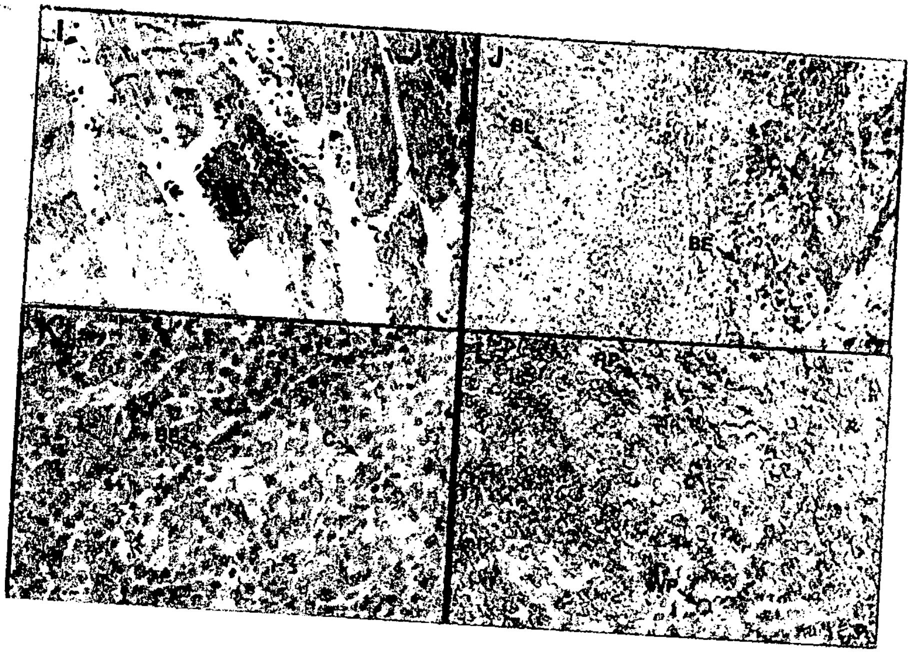

Figure 29 (cont'd)

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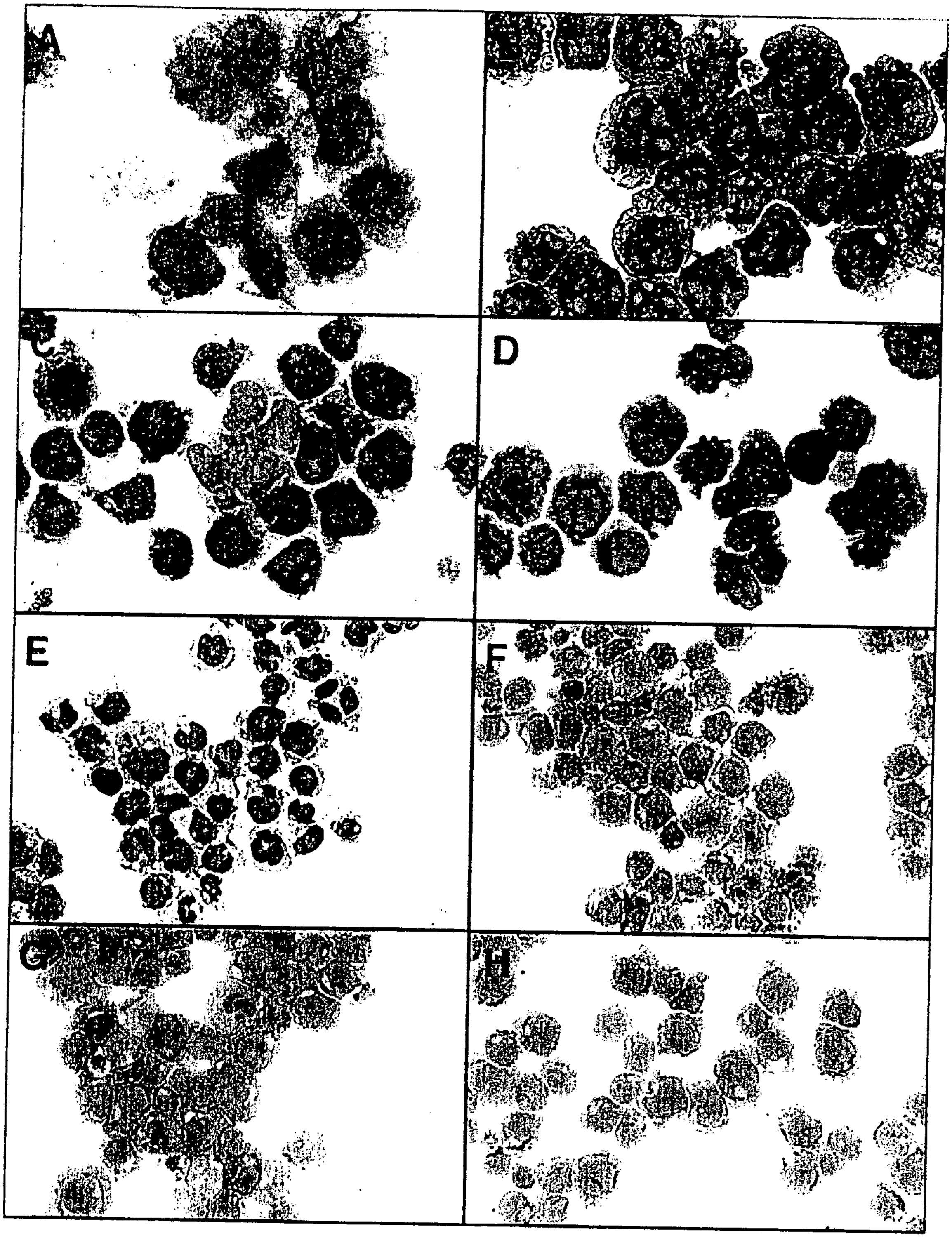

Figure 30

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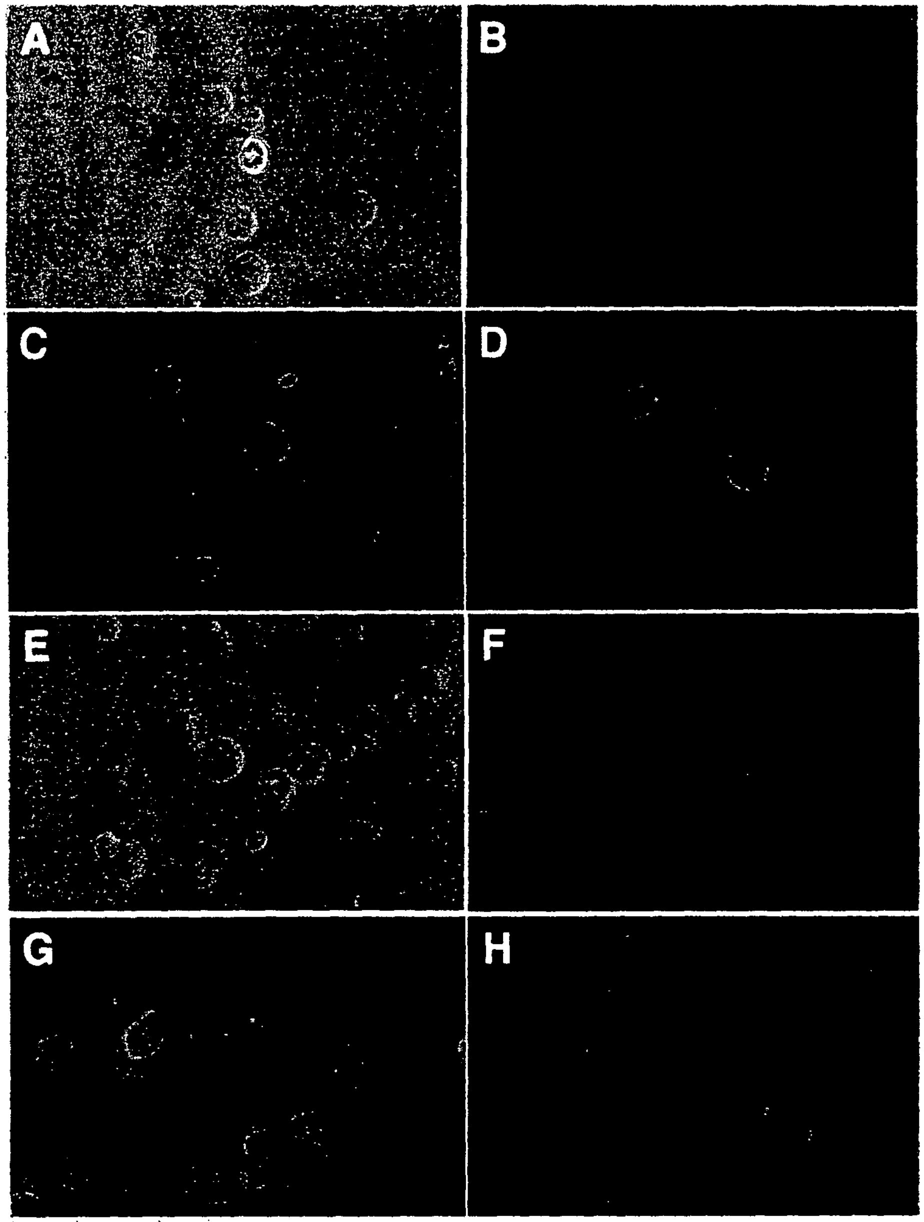

Figure 31

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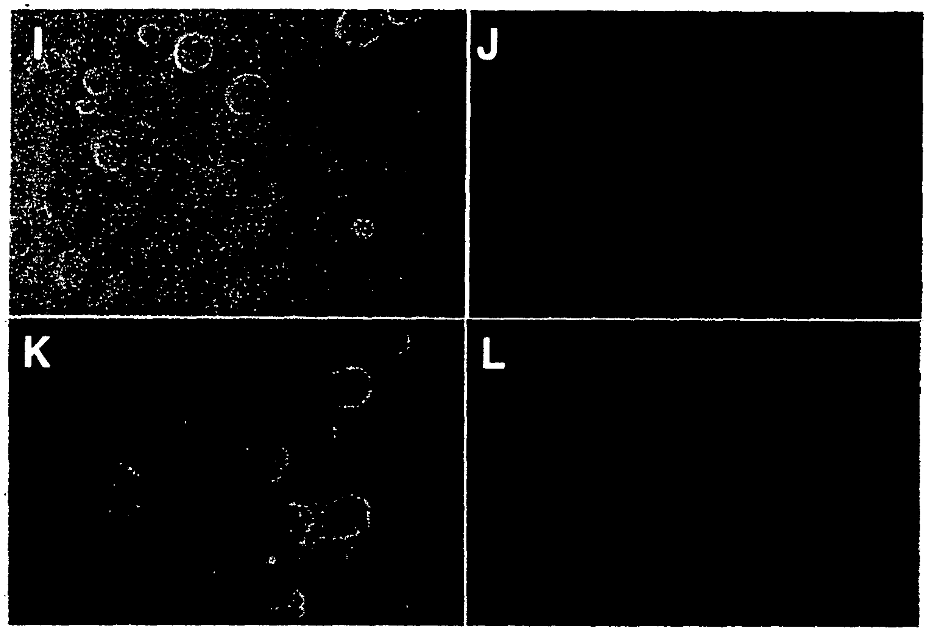

Figure 31 (cont'd)

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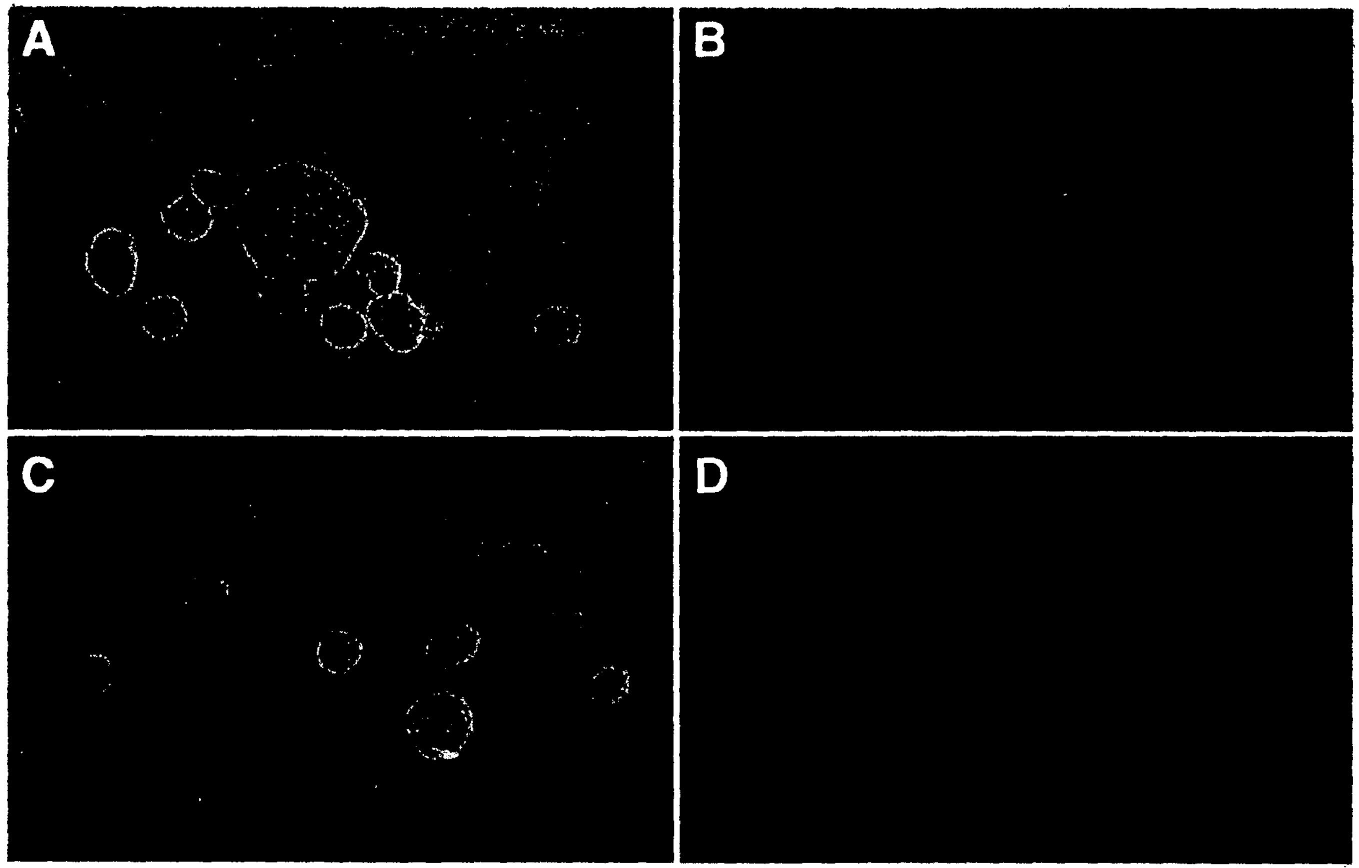

Figure 32

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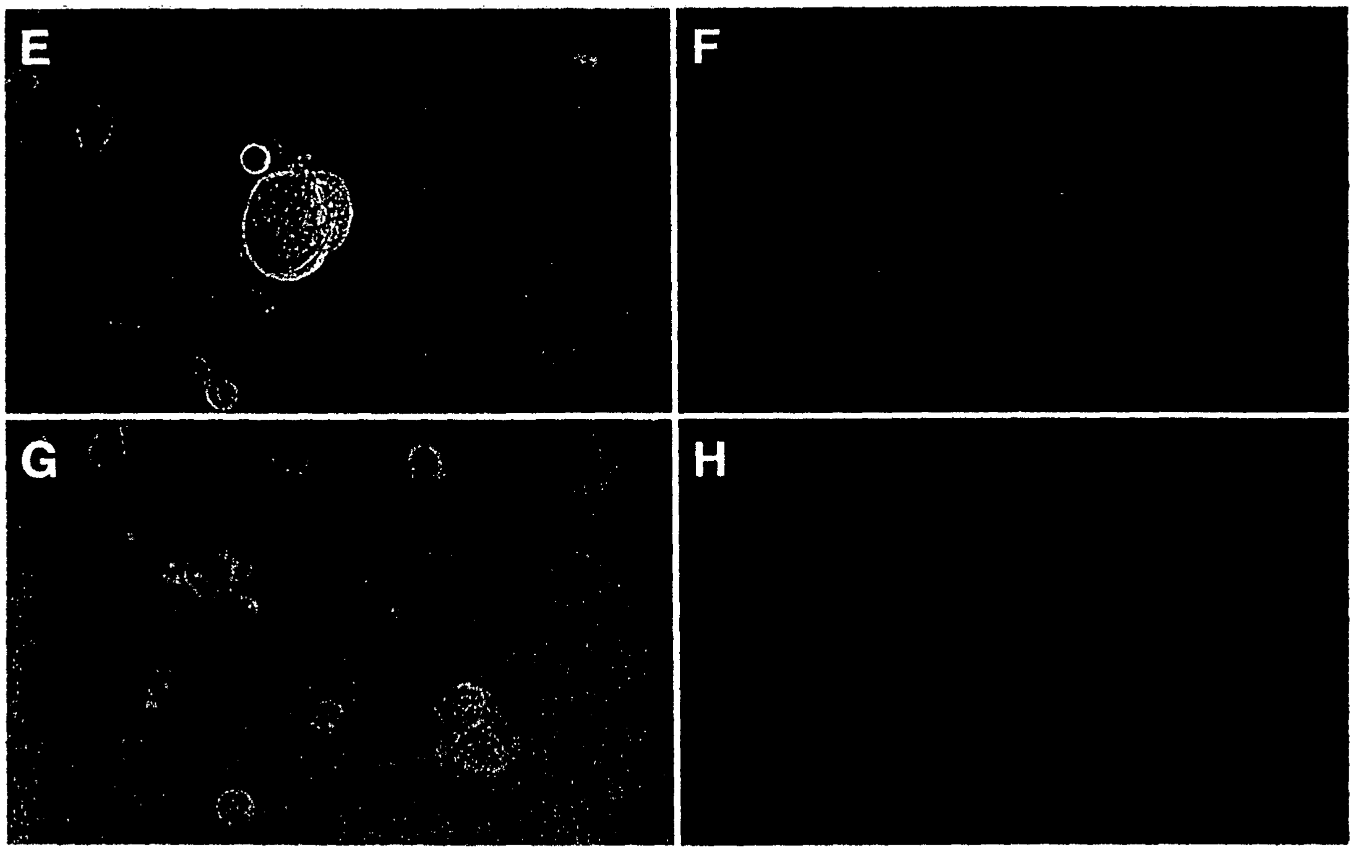

Figure 32 (cont'd)

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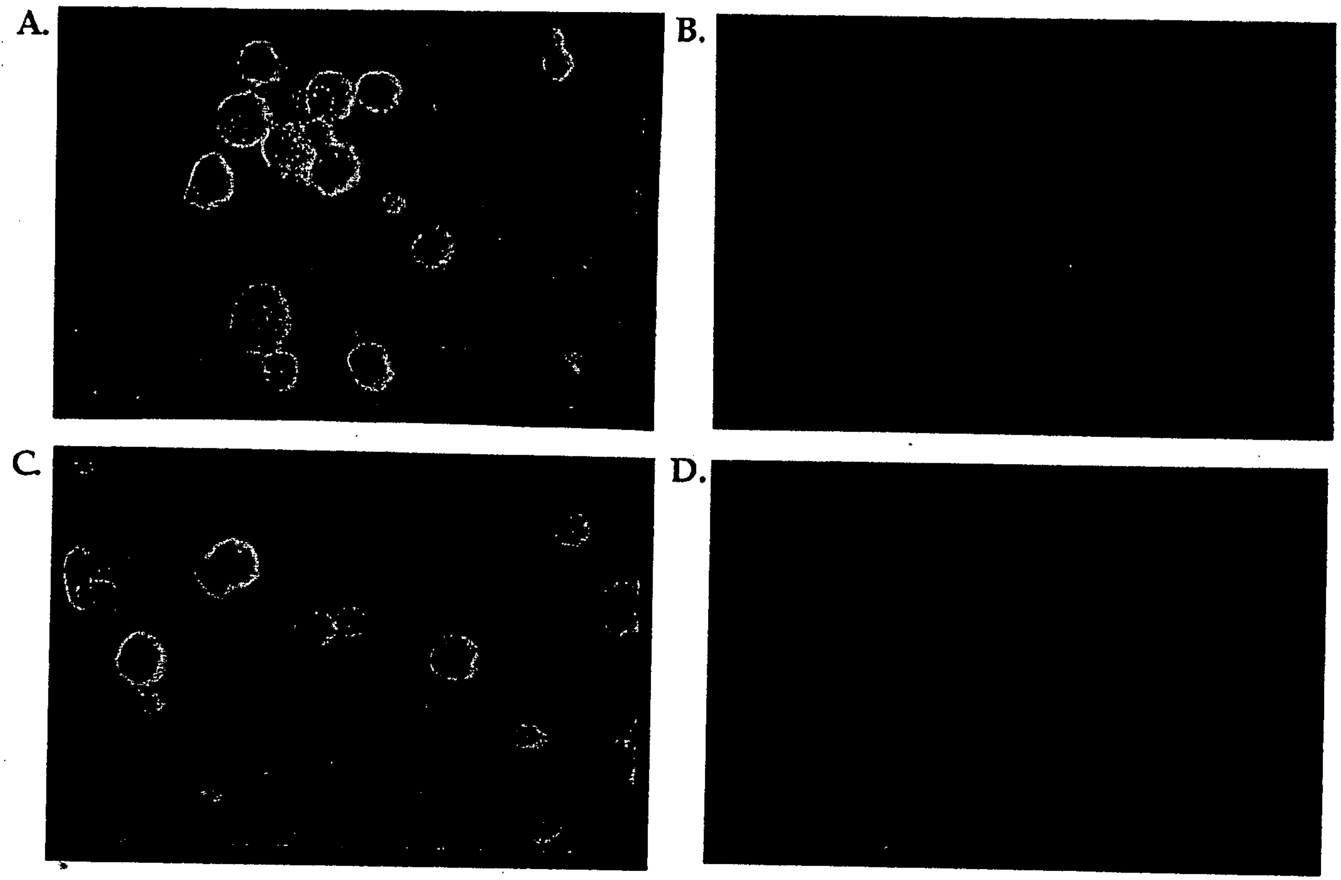

Figure 33

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Additional Oligonucleotide primers used for apo-dystrophin-4 southern blotting and sequencing

FORWARD

GTT CGT TAA TAC AAG TAG	F2.3(@28)	(SEQ ID NO 15)
GCC AAG GTG GAA AAG ATG	F2.2(@73)	(SEQ ID NO 16)
CCA GTA GCC TGA TCC AAC	F3.2(@208)	(SEQ ID NO 17)
GGC TTC ATT AAT AAG	F3.1(@257)	(SEQ ID NO 18)
GGC AAA GAA ACA GAG TG	F4.2(@379)	(SEQ ID NO 19)
CAG GAC ACA ATG TAG GA	F4.1(@449)	(SEQ ID NO 20)
GTT ATA AAG AAA GAA TTA TAA AG	FJn(@846)	(SEQ ID NO 21)
GAA AAT AAC GCA ATG GAC	F5.1(@875)	(SEQ ID NO 22)

REVERSE

GAT GGG ATA CAT CTT TTC C	R6.1(@99)	(SEQ ID NO 23)
CAA GCT ACA TTC AGG TTC CC	F2.2R(@188)	(SEQ ID NO 24)
GGA CTC CAT CGC TCT GCC	R4.1(@510)	(SEQ ID NO 25)
GAC TTA GAA ACT ACT G	R3.4(@694)	(SEQ ID NO 26)
ATA GAC GTG TAA AAC CTG C	R2.1(@735)	(SEQ ID NO 27)
AAC TGT TAT AAA TTT TTA	RSP2(@848)	(SEQ ID NO 28)
CTT TTT CCT TTA TAA TTC TTT C	R2.3$_{o}$(@875)	(SEQ ID NO 29)

Figure 34

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An Additional Splice Product Predicted From The Apo-4 Gene

A second potential theoretical splice product which retains exon 78.3 is shown below.

H2 p1-124 spliced product =351 bp, 117 amino acids + 10 from vector + 1 N-glycosylation site; predicted weight = 21.9 Kd

Figure 35A

Peptide Generated

MFVNTTKVEKMYPIMEYSCSDRNLVLIYGILLIYIYIGNLNMKKEQNKCFTTPDSRMVFII FIQQRGLDSKSLQEINLYFCEGFYTSMQLYKKVIRKLHKITQWTRTPQNQSEVEIA (117 amino acids) (SEQ ID NO 30)

Figure 35B

Start	Exon No.	Exon Position	Exon Length	Intron No.	Intron Position	Intron Length
@26 bp	78.1	@16-41	26 bp	78.3	@42-74	33 bp
	78.3	@75-181	106 bp	79.1	@182-530	349 bp
	79.1	@531-655	125 bp	79.4	@656-721	66 bp
	79.4	@722-770	49 bp	79.55	@771-876	105 bp
	79.55	@877-894	18 bp	79.75	@895-933	39 bp
	79.85	@934-967	33 bp			

Hydrophobicity Scale KD; Candidate membrane-spanning segments:

Certain 1 22- 42 1.8833

Figure 35C

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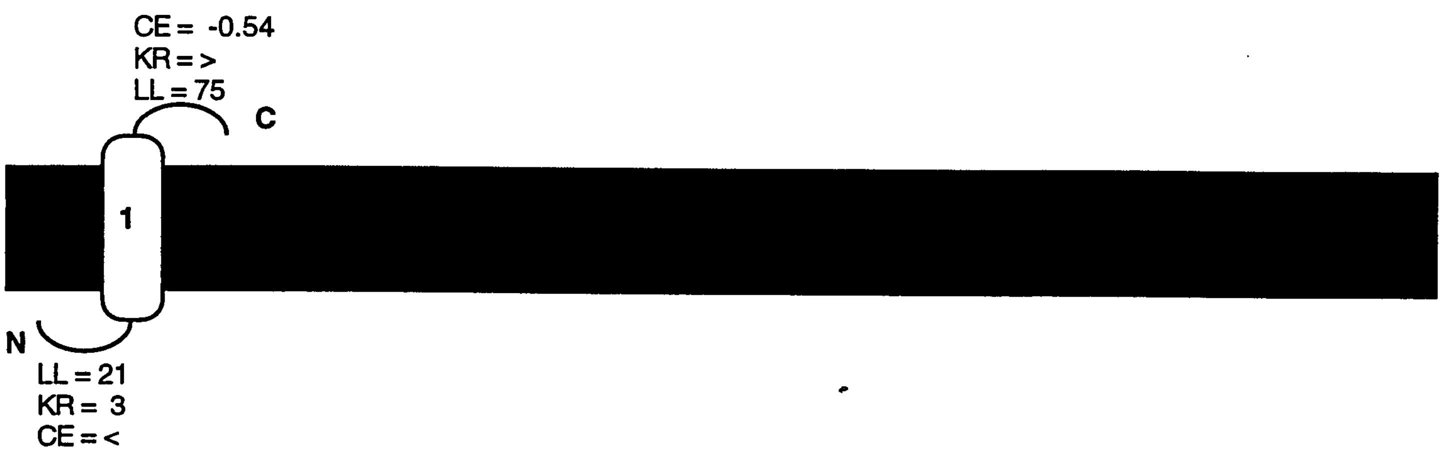
D. Predicted TM structure

> : Too long to be significative
< : Too short to be significative
Ll : Loop length
KR : Number of Lys and Arg

KR Diff : Positive charge difference
CE : Net charge energy
CE Diff : Net charge difference
CH Diff : Charge difference over N-term segments



KR Diff = 3 **CYTOPLASM**
CH Diff = -2 **OUTSIDE**
CE Diff = 0.54 **OUTSIDE**

Structure no. 1

Figure 35D

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Nucleic Acid Subsequence Sites Identified In Apo-4

Motif	Position	Significance
CpG	-7, (+28, +106)	DNA methylation site
CAAT	-132, (+127, +131)	Binding of CAAT factors
TATAAT (5/6)	-120, -114, (+10)	TFIID Binding site
TATA	-154	Binds RNA polymerase II and TFIID
CCATTCA	-162, -131	Cap Site I
TATCAGT	+12, (+25)	Cap Site II
TGGCTGCAAGCCCAA (10/14) (SEQ ID NO: 32)	-57, (+41)	Binds CTF/NF-I protein
GTGATGG	-140, -4, +11, +32	Eucaryotic Transcription Initiation Site

Figure 36

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Top Pred predicts 4-5 transmembrane domains for a full-length apo-4F product in which all the stop codons are suppressed.

Protein sequence and position of predicted TM domains

```
                                                     Begin TM1(R)
                                       P1              |              P2
MFVNTSREKV INQSLIAKVE KMYPIMEYSCSD RNLVLIYGIL LIYIYIGNLN VARHFSMK60

TPVARSNIKL ILTNNVKWLH KKGFASSWKL VKNQTLLCTP SMQLLCCLHP EMGNDFPNGK 120
                                                     P3
ETERCYLSAP FVKSVFLSLC FPGHNVGSLF HMADDLGRAM ESLVSVMTDE EGAEKMFYNS180

RFPHGFYNIH TTKRIRQKEF TRNKSIFLRR VVVLYCRFQK FLSLLLFCKQ WQVLHVYAIV 240

QKSYKKTTCK ILIAKKLAIS LYGTHFGLFK NLKQLKRKNY KGKRKKRNGQ VVKLRTQVCT 300

IIRNTPKPKR GRNSMRSRVR CKLI (324 amino acids) (SEQ ID NO 31)
```

Hydrophobicity Scale KD

Figure 37A

Apo-4F : Candidate membrane-spanning segments:

Certain	1	33- 53	1.9073
Putative	2	93- 113	0.8052
Certain	3	124- 144	1.2552
Putative	4	209- 229	1.1833
Putative	5	246- 266	0.9240

I. Transmembrane segments included in structure 8: **1 2 3 4 5;** Loop lengths: 32 39 10 64 16 58

Figure 37B

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K+R difference: -19; -> Orientation: **N-out**; Charge-difference over N-terminal Membr. segs.

(±15 residues): -3; -> Orientation: **N-out**

CYT-EXT profile (neg. values indicate cytoplasmic preference): < < < < -0.13 <

CYT-EXT difference: 0.13

-> Orientation: **N-out**

II. Transmembrane segments included in structure 7: **1 3 4 5;** Loop lengths: 32 70 64 16 58

K+R profile: 5 > 22 > 5; K+R difference: 22 -> Orientation: **N-in**

Charge-difference over N-terminal Membr. segs. (±15 residues): -3; -> Orientation: **N-out**

CYT-EXT profile (neg. values indicate cytoplasmic preference): < -0.13 < -0.26 <

CYT-EXT difference: 0.13; -> Orientation: **N-out**

Figure 37B (cont'd)

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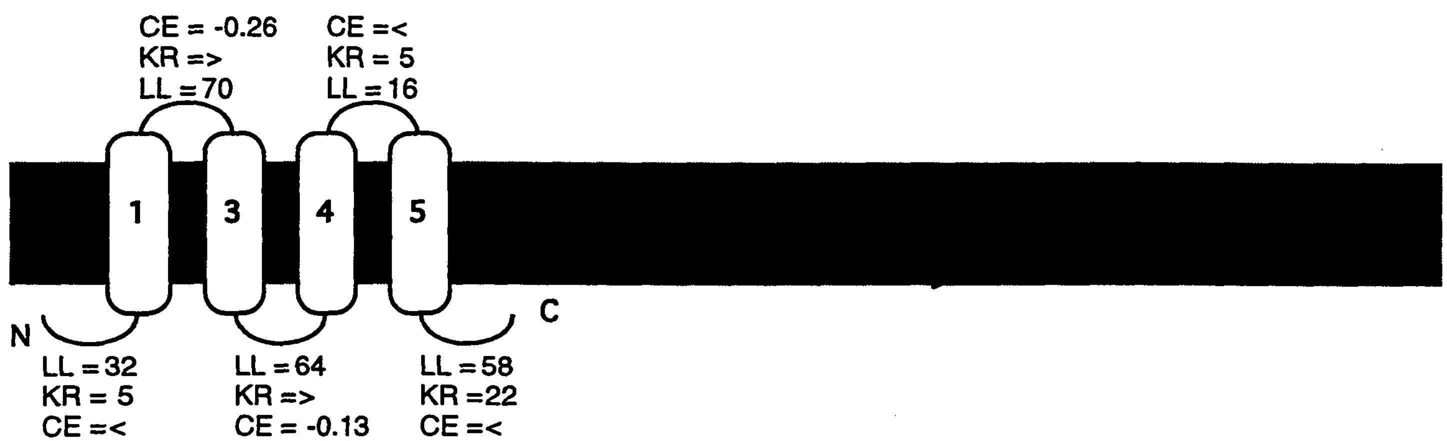
C. TopPred predicts a cytoplasmic N-terminus for four TM domains

> : Too long to be significative
< : Too short to be significative
Ll : Loop length
KR : Number of Lys and Arg

KR Diff : Positive charge difference
CE : Net charge energy
CE Diff : Net charge difference
CH Diff : Charge difference over N-term segments



KR Diff = 22 CYTOPLASM
CH Diff = -3 OUTSIDE
CE Diff = 0.13 OUTSIDE

Structure no. 7

Figure 37C

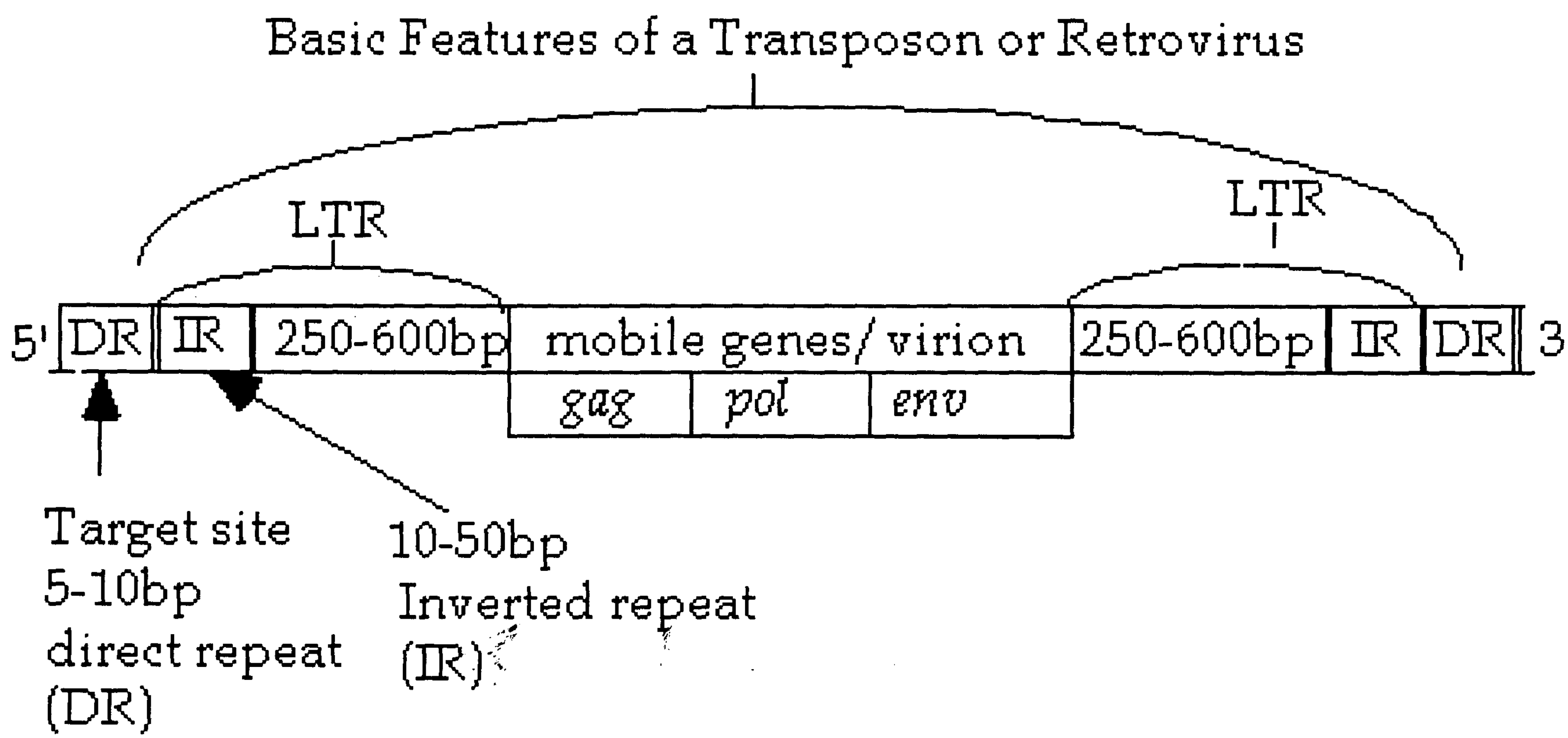


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Figure 38A

Structure of the apo-4 inversion element before rearrangement

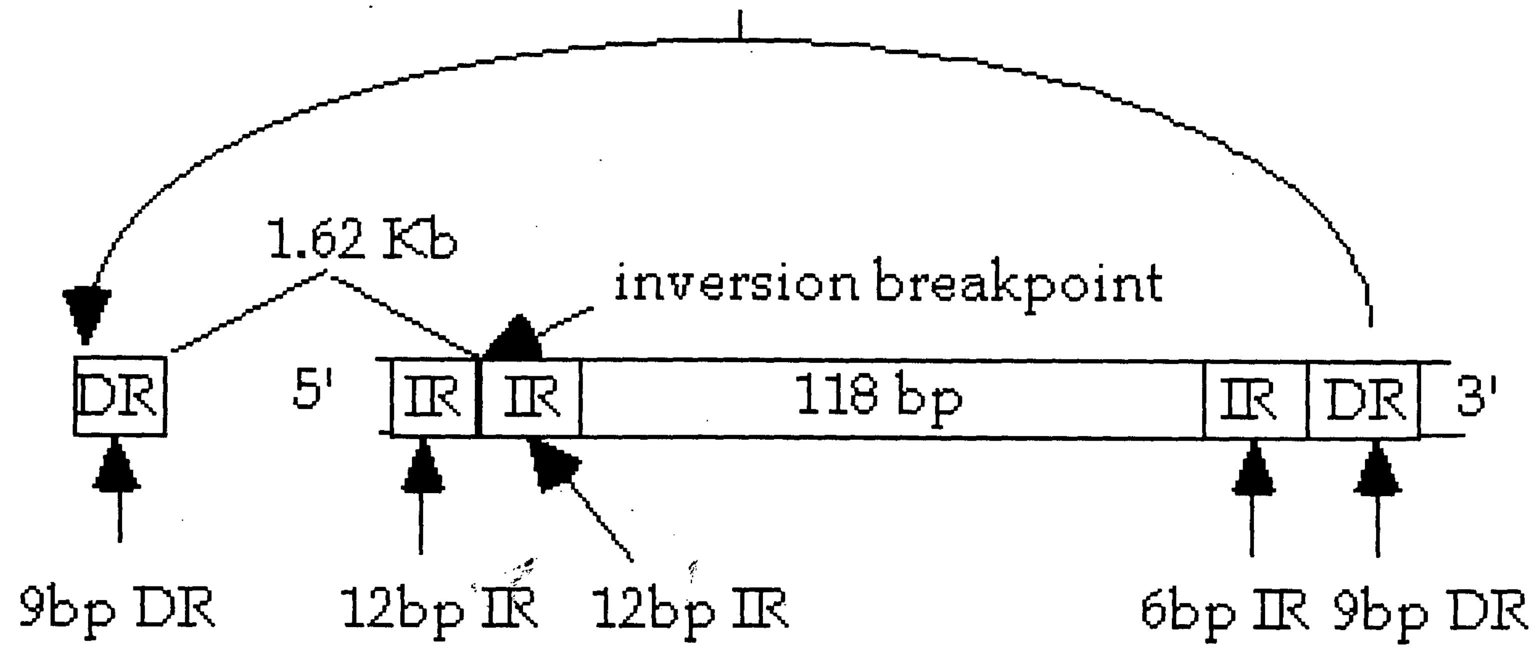

Figure 38B

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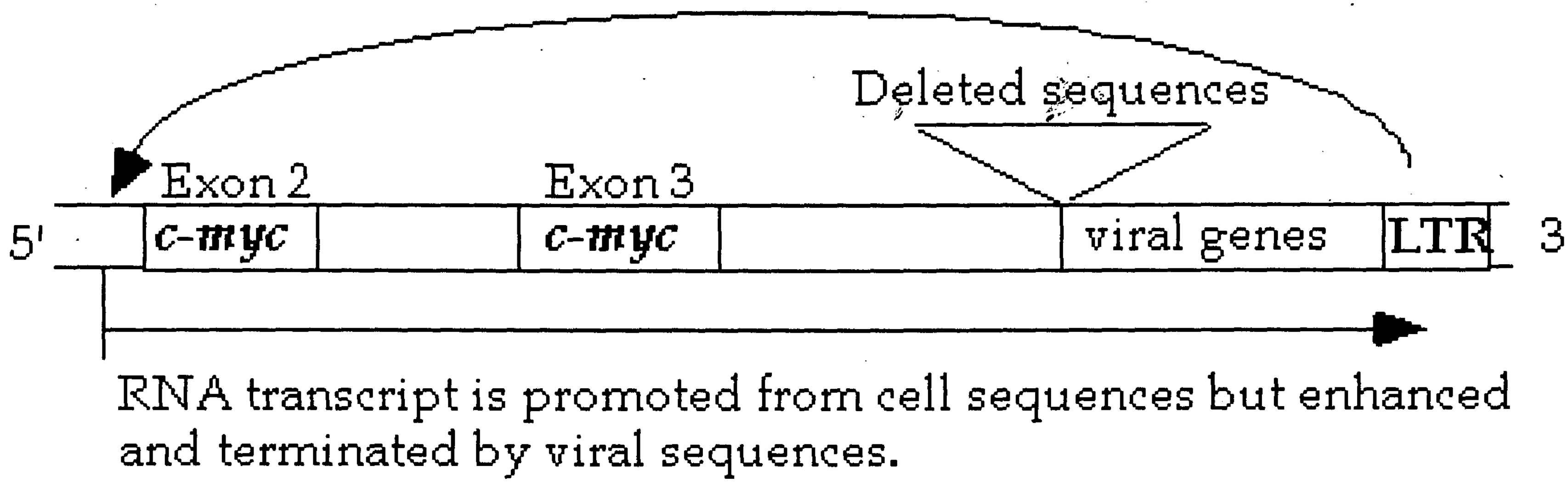

Figure 39A

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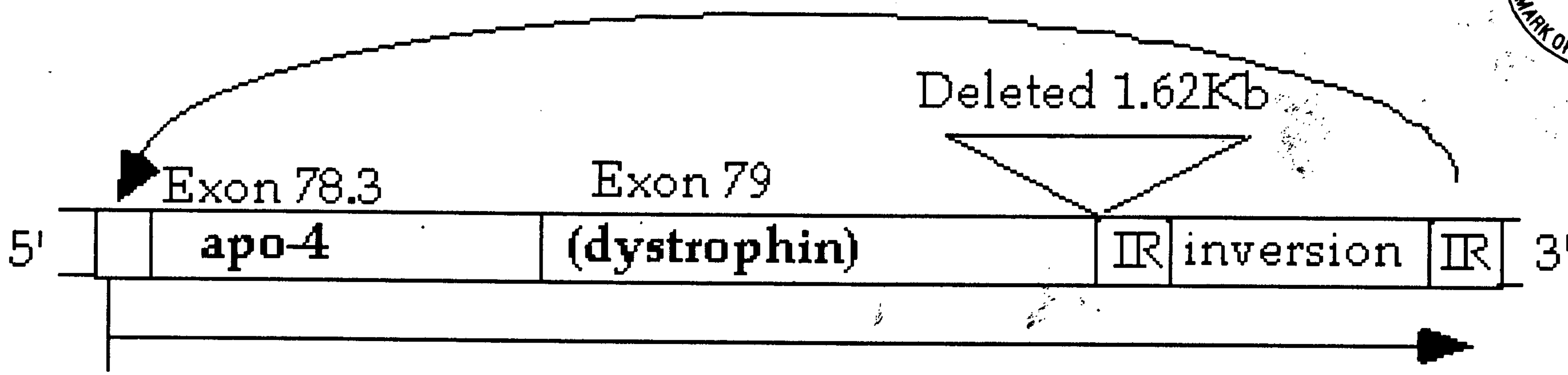

RNA transcript is promoted from cell sequences but enhanced and terminated by inversion sequences which may also activate suppressor tRNAs or reverse transcriptase activity to prevent the recognition of stop codons. Inverted repeats (IR) are present at both ends of the inversion, as they are in retroviruses and transposable elements.

Figure 39B

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